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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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(without alignments)
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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 54, Appl	Sequence 13444, A	Sequence 52, Appl	Sequence 51, Appl	Sequence 557, App	Sequence 47, Appl	48,	Sequence 46, Appl	Sequence 3545, Ap	Sequence 45, Appl	Sequence 855, App	Sequence 8545, Ap	Sequence 16, Appl	Sequence 14, Appl	Sequence 558, App	Sequence 163, App	Sequence 10, Appl	Sequence 2, Appli	Sequence 12, Appl	Description

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DINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAP

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177 7.9 46 9 US-09-813-718-53 146.5 6.5 391 9 US-10-128-714-8379 146.5 6.5 391 9 US-10-128-714-8379 146.5 6.5 339 10 US-09-815-242-11422 142.5 6.3 339 10 US-09-813-718-8 132.5 5.9 372 9 US-09-813-718-2 132.5 5.9 372 9 US-09-815-242-11070 133.5 5.1 423 10 US-09-815-242-10678 113 5.0 415 10 US-09-815-242-12649 113 5.0 420 10 US-09-815-242-12649 113 5.0 420 10 US-09-815-242-12649 113 5.0 420 10 US-09-815-242-12649 110 5.0 345 9 US-09-738-626-4252 110.5 4.9 331 9 US-10-126-927-50 108 4.8 306 9 US-10-126-927-64 108 4.8 306 9 US-10-126-927-64 108 4.8 306 9 US-10-126-927-64 108 4.8 306 9 US-10-126-931A-50 108 4.8 306 9 US-10-126-931A-50 108 4.8 306 9 US-10-126-931A-50 108 4.8 306 9 US-10-126-931A-51 109 4.8 306 9 US-10-126-931A-51 100 4.7 334 10 US-09-815-242-13806 107 4.8 306 9 US-10-126-937-45 108 4.7 336 9 US-10-126-937-45
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ALIGNMENTS

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RESULT 1
US-09-813-718-12
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APPLICANT: Schimmel, Paul
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 2246;
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 424; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 437
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human
OTHER INFORMATION: TrpRS in pET20B
                  181
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                                                                                       121 AMHVGHLIPFIFTKMLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGF 180
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                                                                                                                                                                               61 GSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSE 120
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DINKTEIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAP 240
                                                             AMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGF 180
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Pred. No. 2.1e-203;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-126-467B-2
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US-10-126-467B-2
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Paley, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10126467B Publication No. US20030059797A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ANIMAL MODEL OF AND TEST FOR ALZHEIMER'S DISEASE FILE REFERENCE: PALL-111

CURRENT APPLICATION NUMBER: US/10/126,467B

CURRENT FILING DATE: 2002-11-19

PRIOR APPLICATION NUMBER: 60/284,980

PRIOR FILING DATE: 2001-04-19

PRIOR FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: 09/513,895

PRIOR APPLICATION NUMBER: 09/513,895

PRIOR APPLICATION NUMBER: 09/384,869

PRIOR APPLICATION NUMBER: 09/384,869

PRIOR APPLICATION NUMBER: 09/384,869

PRIOR APPLICATION NUMBER: 09/384,869

PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-08-27
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RESULT 4
US-09-919-039-163
; Sequence 163, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
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Publication No. US20020182666A1

GENERAL INFORMATION:

APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221

FULE REFERENCE: 00-221

CURRENT APPLICATION NUMBER: US/09/813,718

CURRENT FILING DATE: 2001-03-21

NUMBER OF SEQ 1D NOS: 58

SOFTWARE: Patentin Ver. 2.0

SEQ 1D NO 10
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Best Local Similarity
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ORGANISM: Artificial Sequence
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Pred. No. 2.4e-203;
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 558
LENGTH: 475
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CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
RUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 163
LENGTH: 471
LENGTH: 471
                                                                                                                                                                                                                                                                Sequence 558, Application US/09925302 Patent No. US20020044941A1
GENERAL INFORMATION:
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FEATURE:
RAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 2705515CD1
--09-919-039-163
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LENGTH: 475
TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 6.1e-202;
0; Mismatches 2;
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; ORGANISM: Artificial Sequence; FEATURE; OTHER INFORMATION: Description; OTHER INFORMATION: supermini US-09-813-718-14
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                                                                                                                        Best Loc
Matches
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SEQ ID NO 14
LENGTH: 415
TYPE: PRT
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CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
                                                                                                                      Local Similarity 100.0%; P. Cocal Similarity 0;
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                   FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 143
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                                                                                                                                      94.2%; Score 2116; DB 9; 1 100.0%; Pred. No. 3.6e-191;
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Pred. No. 6.2e-202;
                                                                                                                         Mismatches
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                                                                                                                                                                                                                 Sequence: human
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                                                                                                                                                   Length 415;
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US-09-813-718-16
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Best Local Similarity
Matches 378; Conserv
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CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/09813718
Publication No. US20020182666A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase
TITLE OF INVENTION: The Regulation of Angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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  302
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  CDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVT
                    CDVDVSFMYLTFFLEDDDXLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVT
                                                                                                                                                     CIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPA
                                                                                                                                                                                   CIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPA
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                                                                                                                                                                                                                                                                                                               KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYG
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                                                                                                                                                                                                                                                                                                                                                                                                                  SAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAYENK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
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100.0%; Pred. No. 3.9e-179;
tive 0; Mismatches 0;
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TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8545
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CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
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Best Local Similarity
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APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
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PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
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                                                                                                                                                                                                                                                                                                                                                                                                                                61 RISKELLERFERVTGRRPHRFMRRGIVFSHRDLNLILDRYEKGQPFYLYTGRGPSSDSMH
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LSF 421
                                                                                                                                                                                                                                SNSFPQIF-RDR---TDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFFALQG
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                                                          FLEDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRK 418
                                                                                                                                         AQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTF
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                                      FMEDDEELERIRVAYEKGEMLTGEVKQKCIAELQAYVQAFQERRAQVTDEIVAEFMRPRS
                                                                                                                 PGSKMSASVETSAIFMNDAPNRIKNKINKYAFSGGQDTAELQROLGANTKDDVPFQYLTF
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APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Methods of Use
                     50.3%; Score 1129.5; DB 53.7%; Pred. No. 4.4e-98
Mismatches 115; Indels
                                          DB 9;
                                          Length
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US-09-813-718-45
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                                                                              ; ORGANISM: Homo sapiens
US-09-813-718-45
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NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 855
LENGTH: 173
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                     Sequence 45, Application US/09813718 Publication No. US20020182666A1 GENERAL INFORMATION:
                      Query Match
Best Local Similarity
                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 156;
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                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                              APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
                                                                                                                                                                                                                                                                                                               APPLICANT: Schimmel, Paul APPLICANT: Wakasugi, Kei
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PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                       TYPE: PRT
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OTHER INFORMATION:
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OTHER INFORMATION: Xaa equals any of the naturally
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                                                                                                                                       ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 DLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQI 249
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      85;
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      Conservative
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98.7%;
100.0%;
20.4%; Score 458; UB 3, 100.0%; Pred. No. 9.5e-36; 0;
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                                        Length 85;
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US-09-813-718-46
; Sequence 46, Application US/09813718
; Publication No. US20020182666A1
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-3545
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Best Local Similarity
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APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
TILE REFERENCE: 00-221
CURRENT ENLING NAME: 00-03-21
NUMBER OF SEQ ID NOS: 58
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PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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NUMBER OF SEQ ID NOS: 8603
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APPLICANT: Exoshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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US-09-813-718-48
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US-09-813-718-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Oryctolagus cuniculus 
US-09-813-718-48
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 85
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publication No. US20020182666A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
                                                                 SEQ ID NO 47
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ORGANISM: Mus musculus
-09-813-718-47
                                                                                 CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                    APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase
TITLE OF INVENTION: The Regulation of Anglogenesis
FILE REFERENCE: 00-221
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/813,718
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                                TYPE: PRT
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                                                LENGTH: 85
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88.1%;
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Pred. No. 4.3e-30
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Pred. No. 8.7e-27;
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NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 557
LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-925-302-557
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                                                                                                                                                                               ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-557
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APPLICANT: Rosen et al.
APPLICANT: INVENTION: Nucleic Acids, Proteins and Antibodies
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Patent No. US20020044941A1
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US00/05918
                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (142)
                                                                                                                                                                                                                                             LOCATION: (137)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
                                                                                                                                                                                                                                                                                         LOCATION: (130)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                      LOCATION: (124)
OTHER INFORMATION: Xaa
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LOCATION: (124)
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                           61 GSSKIDKELINRIERATGQRPHHFLRRGIFF 91
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Search completed: July 10, 2003, 12:33:36 Job time : 22.5855 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.

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Minimum
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA198.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT:
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA290.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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392	392	415	415	471	475	484	484	437	437	Length	
23	22	23	22	20	21	23	22	23	22		
AAE13494	AAB47618	AAE13493	AAB47617	AAY05372	AAB58220	AAE13491	AAB47615	AAE13492	AAB47616	ID	
Human inactive try	Human inactive Tro	Human supermini tr	Human supermini Tr	Human HCMV inducib	Lung cancer associ	Human tryptophanyl	Human full-length	Human mini tryptop	Human mini TrpRS.	Description	

45	44	43	42	41	40	39	38	37	36	35	ω 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
120.5	122.5	123	126.5	128	132.5	132.5	132.5	132.5	134	134	134.5	138.5	146	152	158.5	159.5	162.5	164.5	174.5	182.5	185.5	185.5	203.5	256	356.5	458	803	831	968	1218.5	1304	1304	1378	1378
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~		Arabidopsis thalia	Listeria monocytog	Haemophilus influe	Human tyrosyl t-RN	ful1	mini	mini		Human mini TyrRS m	Drosophila melanog	Arabidopsis thalia	Helicobacter pylor		Putative P. abvesi	rotein inv	albicans		Lactococcus lactis		Streptococcus pneu	Tryptophanyl tRNA	Streptococcus polv	Human tryptophanyl	Lung cancer associ		ive P.		Arabidopsis thalia	Tryptophanyl-tRNA		Arabidopsis thalia		Drosophila melanog

ALIGNMENTS

RESULT 1

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AAB47616
                                                                                                                                                                                                                  Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucoyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization;
WPI; 2001-626377/72.
N-PSDB; AAH43603.
                                   Schimmel P, Wakasugi K;
                                                                                 31-MAR-2000; 2000US-193471P.
                                                                                                           21-MAR-2001; 2001WO-US08966.
                                                                                                                                    11-OCT-2001
                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                         07-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                      AAB47616 standard; Protein; 437 AA.
                                                                                                                                                           WO200174841-A1
                                                                                                                                                                                                          tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
                                                                                                                                                                                                                                                                                               Human mini TrpRS.
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RESULT 2
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12-FEB-2002
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              AAE13492 standard;
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                                421 FDFQ 424
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                                       FDFQ 424
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(first
                                                                                                                                                                   AA,
              Protein;
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decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel. The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo balton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or a solid tumor. Disclosure; Page 123-24; 150pp; English angiogenesis, New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating tumor metastasis and treating myocardial infarction

DINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAP GSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSE AMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGF GSSKIDKELINRIERATGORPHHFLRRGIFFSHRDMNOVLDAYENKKPFYLYTGRGPSSE EDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARKEVTDEIVKEFMTPRKLS EDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARKKEVTDEIVKEFWTPRKLS TKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFL TKMSASDÞNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFL SFSNSFPQIFRORTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQ SESNS PPQIERDRIDIQCLIPCAIDQDPY FRMIRDVAPRIGY PKPALLHSIFF PALQGAQ DINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAP AMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVENÅKDIIACGF 100.0%; Score 2246; DB 22; 100.0%; Pred. No. 7.4e-222; tive 0; Mismatches 0; DB 22; Indels Length 437; 0 Gaps 300 300 240 180 120 60 420 420 360 240 180

Human mini tryptophanyl t-RNA synthetase in pET20B

TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venues ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy. Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase;

Homo sapiens.

WO200175078-A1

21-MAR-2001; 2001WO-US08975

31-MAR-2000; 2000US-193471P

(SCRI) SCRIPPS RES INST

Schimmel P, Wakasugi

N-PSDB; AAD22483 2002-010784/01

Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, useful for treating solid tumor or suppressing tumor metastasis in

Example 1; Page 123-124; 149pp; English

CC truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann CC fold nucleotide binding domain and polynucleotides encoding them. The CC fold nucleotide binding domain and polynucleotides encoding them. The CC sequences are useful for regulating vascular endothelial cell function, preferably angiogenesis. Angiogenic TrpRS sequences are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure CC sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS cequences can also be used in plastic surgery when reconstruction is CC angiogenic TrpRS is also used in pastic surgery when reconstruction is CC angiogenic TrpRS is also used in association with surgery and following the damage of myocardial infarction and in CC conjunction with coronary bypass surgery by stimulating the growth of CC crimbunoassays to detect the presence of tumours. They are also used in conjunction with angiography. TrpRS antibodies are useful for blocking endogenous angiogenic activity and retard the growth of CC solid tumours. These antibodies may also be used to treat inflammation CC solid tumours. These antibodies may also be used to treat inflammation CC solid tumours. These antibodies may also be used to treat inflammation CC passed by increased vascular permeability. Inhibiting the activity of CC propriatis, diabetic retinopathy, all of which are characterised by complant treats. The present sequence is human truncated tryptophanyl t-RNA synthetase (mini TrpRS; residues 48-471 of cull-length TrpRS protein) protein in pET20B. The patent discloses human aminoacyl tRNA synthetases, particularly

Sequence 437 A,

Matches Query Match Local Similarity Conservative 100.0%; 0; Score 2246; DB 23; Pred. No. 7.4e-222; Mismatches 0; Indels Length 437; 0

밁 S MSYKAAAGEDYKADCPPGNPAPTSNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRF 60 60

GSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSE 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte estatase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-trNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of
                                                                                                                                                                                                                             New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction -
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                                                                                                                                                                             Disclosure; Page 117-19;
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Best Local Sim
Matches 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      full length TrpRS with polymorphonuclear leucocyte elastase. Truncated TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA wall of the blood vessel.
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Human tryptophanyl t-RNA synthetase (TrpRS) in pET20B

12-FEB-2002

(first

entry)

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X Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase; TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; diabetic

Homo

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realing agents for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. TTPRS sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Angiogenic TrpRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft conjunction with coronary bypass surgery by stimulating the growth of conjunction with coronary bypass surgery by stimulating the growth of conjunction with surgery is also used in conjunction with angiography. TrpRS DNAs are useful in gene therapy. TrpRS antibodies are useful in gene therapy and retard the growth of conjunctions. These and solve and retard the growth of condit tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of crops by antisense technology is useful for preventing further growth is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or even regress solid tumours, and for treating rheumatoid arthritis, psoriasis, diabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human tryptophanyl
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Pred. No. 8.7e-222;
; Mismatches 0;
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             chromosome identification, as chromosome markers, and for numerous otl diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds ar infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                            Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58166 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; r
                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-587514/55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; lung cancer associated protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lung cancer associated polypeptide sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                   y cancer associated gene sequences, igens, useful for treatment, prevent
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                                                                                                                                                                                                                                                                                                                                                Page 1052-1053; 1425pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                     prevention,
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tion, and diagnosis of disorders
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                                                WPI; 1999-243729/20
N-PSDB; AAX33942.
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08-SEP-1997;
                                                                                                                                                                                                                                                                                                                08-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCMV inducible gene; cig; human; human cytomegalovirus; interferon; anti-viral therapy; anti-HCMV therapy; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human HCMV inducible gene protein, SEQ ID NO 12.
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Pred. No. 2.9e-220;
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Matches 421
                                                                                                           Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes (crg or crgs). The products can be used to obtain agents which (be used for anti-viral therapy, particularly anti-HCMV therapy. They calso be used for the development of drugs that would allow for higher dosage IFN treatments without the concomitant toxicity normally associated with administering high levels of IFN. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is encoded by a human gene of the invention, and is induced to express by both HCMV and interferon (IFN), designated HCMV-inducible genes (cig or cigs). The invention also relates to genes that are repressed in the presence of HCMV infection, designated HCMV-repressible
                                                                                                        tryptophanyl-tRNA
                                                                                                                                                                                                                                                                                                                          Human supermini TrpRS.
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Pred. No. 9.5e-220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC the invention comprises a Rossmann fold nucleotide binding domain, and capable of regulating vascular endothelial cell function. It is of capable of regulating vascular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated CC TrpRS is useful for regulating angiogenesis, tumor metastasis, ce enhancing angiogenesis to a graft, treating myocardial infarction, combined the strong and a condition that would benefit from increased or complete in diagnosis and as a wound benefit from increased or complete strong and allocars, diabetic ulcers, burns and injuries and in ce plastic surgery when reconstruction is required following a burn or complete surgery when reconstruction is required following a burn or complete surgery enter there is high risk of infection. Truncated TrpRS conjunction with angiography to administer the angiogenic tRNA conjunction with angiography to administer the angiogenic tRNA capable or polynucleotides directly to the lumen and content of the blood vessel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schimmel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-193471P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 129-30; 150pp; English
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                     KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
                                                                       KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
                                                                                              KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
                                                                                                                                                                                IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
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                                                                                                                                              IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 AA;
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Pred. No. 1.6e-208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 129-130; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD22484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase; TyrRS; vascular endothelial cell function; angiogenesis; wound healin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human supermini tryptophanyl t-RNA synthetase in pET20B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCRI ) SCRIPPS RES INST
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CC truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann CC fold nucleotide binding domain and polynucleotides encoding them. The CC invention also relates to tyrosyl t-RNA synthetases (TyrRS). TrpRS CC sequences are useful for regulating vascular endothelial cell function, CC preferably angiogenesis. Angiogenic TrpRS sequences are useful as wound CC healing agents for re-vascularising damaged tissues. They are useful as wound CC treating full-thickness wounds (e.g. dermal ulcers, including pressure CC sequences can also be used in plastic surgery when reconstruction is CC required following a burn, other trauma, or even for cosmetic purposes. CC Angiogenic TrpRS is also used in association with surgery and following the damage of mycardial infarction and in CC surgery and for repairing the damage of mycardial infarction and in CC transplanted tissue. TrpRS is also used in conjunction with angiography. CT TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in complex processes to detect the presence of tumours. They are also useful for blocking endogenous angiogenic activity and recard the growth of CC caused by increased vascular permeability. Inhibiting the activity of psociasis, diabetic retinopathy, all of which are characterised by antisense technology is useful for preventing further growth of CC processed continopathy, all of which are characterised by absorbed in truncated to treatinopathy. The process bunnal anciogenesis. The present segmence is bunnan truncated to abnormal anciogenesis. The present segmence is bunnan truncated to abnormal anciogenesis. abnormal angiogenesis. The present sequence is human truncated tryptophanyl t-RNA synthetase (supermini TrpRS; residues 71-47 full-length TrpRS protein) in pETZOB. The patent discloses human aminoacyl tRNA synthetases, particularly

Sequence

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing dermal ulcer; diabetic ulcer; endothelialization;
                            Disclosure; Page 135-36;
                                                                                 angiogenesis,
                                                                                                     New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating
                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-193471P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
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                                                                                                                                                                                                                                                                   Wakasugi K;
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                                                                               and treating myocardial infarction
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The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated TrpRS is useful for regulating angiogenesis, tumor metastasis, challed the polymorphonuclear leucocyte elastase or conlancing angiogenesis to a graft, treating myocardial infarction, condition, and a condition that would benefit from increased or decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds cuseful in diagnosis and as a wound healing agent for treating wounds concentic surgery when reconstruction is required following a burn or for commetic surgery when reconstruction is required following a burn or conscribed surgery when reconstruction is required following a burn or conscribed surgery when reconstruction is required following a burn or conscribed surgery when reconstruction is required following a burn or conscribed surgery when reconstruction is required following a burn or conscribed surgery when reconstruction is required following a burn or conscribed surgery when reconstruction is required following a burn or conscribed surgery when reconstruction is required following a burn or conscribed surgery and is used in conjunction with angiography to administer the angiogenic tRNA conscribed for polynucleotides directly to the lumen and conscribed the blood vessel.
Sequence
392 AA;
                                                                                                                                                                                                                                TrpRS
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문 Ś 밁 δ В Ś 밁 δ 밁 δ 밁 Ş 밁 S Query Match Best Local Sim Matches 378; 362 407 302 347 242 287 182 227 122 167 107 62 47 N Similarity CIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPA KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYG SAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAYENK DEIVKEFMTPRKLSFDFQ CDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGBLKKALIEVLQPLIAEHQARRKEVT CIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPA DAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSD SAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAYENK DEIVKEFMTPRKLSFDFQ CDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVT LLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGN LLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGN DAVENAKDITACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSD KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYG Conservative 88.5%; 100.0%; 379 0, Score 1988; DB 22; Pred. No. 2.2e-195; Mismatches 0 Indels Length 0 Gaps 406 346 226 166 61 241 286 181 361 301 121 0

RESULT 10
AAE13494
ID AAE13
XX AE13
AC AAE13
XX LI2-FE
XX Human
XX Human
XX Human
XW TYPRS
KW TE-val
KW Te-val
KW Te-val
KW TAUBAN
KW TE-val

12-FEB-2002

(first

entry)

AAE13494 standard;

Protein;

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TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; wenous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability;

rheumatoid arthritis; psoriasis; diabetic retinopathy

Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase; TyrRS; vascular endothelial cell function; angiogenesis; wound healing

Human inactive tryptophanyl t-RNA synthetase in pET20B

Homo sapiens

WO200175078-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ct truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann CC invention also relates to tyrosyl t-RNA synthetases (TyRS). TrpRS CC sequences are useful for regulating vascular endothelial cell function, cc preferably angiogenesis. Angiogenic TrpRS sequences are useful for regulating vascular endothelial cell function, cc preferably angiogenesis. Angiogenic TrpRS sequences are useful for tregulating vascular endothelial cell function, cc treating full-thickness wounds (e.g. dermal ulcers, including pressure cc sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS cs sequences can also be used in plastic surgery when reconstruction is crequired following a burn, other trauma, or even for cosmetic purposes. CC Angiogenic TrpRS is also used in association with surgery and following ct the repair of cuts, for promoting endothelialisation in vascular graft cs surgery and for repairing the damage of myocardial infarction and in cc onjunction with coronary bypass surgery by stimulating the growth of cransplanted tissue. TrpRS is also used in conjunction with angiography. CT TrpRS DNAs are useful in gene therapy. TrpRs antibodies are useful conjunction with angiography. CC solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TrpRS by antisense technology is useful for preventing further growth of conjunction with angiogenesis. The present sequence is human inactive tryptophanyl t-RNA synthetase (TrpRS) in pET20B.
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Best Local Similarity
Matches 378; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses human aminoacyl tRNA synthetases, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 135-136; 149pp; English
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LLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGN 346
                                                                           CIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPA 286
                                                                                                                              DAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSD
                                                                                                                                                       DAVENAKDI I ACGFDI NKT FI FSDLD YMGMSSGFYKNVVKI QKHVT FNQVKGI FGFTDSD
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                                        CIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPA
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Pred. No. 2.2e-195;
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                                                         Matches
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                                                                                 Query Match
                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                              Sequence
                                                                                                                                                      The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 20655; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                    genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                      ccification, but was obtained in electronic
ftp.wipo.int/pub/published_pct_sequences.
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DTKETVVEGVEALTLINGKPDAEPVETGTDAQAQEGATAPTEDVVDPWNVASSNDAGVDYD
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                                                      64;
                                                      Score 1378; DB 22;
Pred. No. 1.3e-132;
4; Mismatches 85;
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                                               The invention relates to an isolated nucleic acid detection reagant capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0176-ABL30511), expressed DNA sequences (ABL0175) and the encoded proteins
                            sequences (ABL01840 (ABB57737-ABB72072)
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11-JUL-2000; 2000US-0614150.
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DB; ABL11306.
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         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                      AAG23697 standard;
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67; Mismatches 87;
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                                                                    LIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
                  Conservative
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Pred. No. 5.4e
57; Mismatches
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5.4e-125;
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S-0144335. S-0144352. S-0144632.

S-0147204 S-0147302 S-0147302 S-0147426 S-0147433 S-0147433 S-0148341 S-0148341 S-0148341 S-014935 S-014935 S-0149372 S-0149372 S-0149372 S-0149372 S-0149372 S-014937 S-014937 S-015086 S-0151086 S-0151086 S-0151086 S-0151088
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Matches 226; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding Candida cytoplasmic tryptophanyl-tRNA (ctRNA) synthetases, useful for producing recombinant ctRNA synthetases and detecting inhibitor of Candida ctRNA synthetase function -
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386 ALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSF 421
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                                                 NKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKK 385
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                               1218.5
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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        US-08-876-885-26
US-08-928-100-2
US-09-425-666-2
US-09-425-666-2
US-09-425-666-2
US-08-743-130A-39
US-08-743-130A-2
US-08-705-868-4
US-09-123-615-4
US-09-123-615-4
US-09-123-616-2
US-09-131-32-2
US-09-131-2
US-09-134-001C-5141
US-08-465-95A-4
US-08-465-994C-4
US-08-96-145-4
US-08-96-145-4
US-08-96-145-4
US-08-96-145-4
US-08-96-145-4
US-08-96-145-4
US-08-966-145-4
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Sequence 26, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 39, Appli
Sequence 39, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 11, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 29, Appli
Sequence 4, Appli
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Sequence 4701, Appli
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Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
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RESULT 1	45 86.5	44 87	43 87	42 87	41 87		39 87	38 87	37 87.5	36 88	35 88	34 88.5	33 89	32 89	31 89.5		29 89.5		
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ALIGNMENTS	US-09-157-257-4	PCT-US93-04692-2	PCT-US93-04384-18	US-09-494-151-2	US-08-331-625A-2	US-09-134-001C-4511	US-09-494-151-43	US-08-331-625A-43	US-08-890-865A-10	US-09-204-764-3 ·	US-08-883-534-3	US-09-157-257-8	PCT-US94-01624-31	US-08-082-849B-31	US-08-101-593-2	US-08-966-145-2	US-08-465-994C-2	US-08-465-995A-2	
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/876,885 FILING DATE: 16-JUN-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: BFOOK, DAVID E. REGISTRATION NUMBER: CP197-02 REFERENCE/DOCKET NUMBER: CP197-02 REFERENCE/DOCKET NUMBER: CP197-02 TELECOMUNICATION INFORMATION: TELEPHONE: (781) 861-6240 TELEPAX: (781) 861-9540 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: US-08-876-885-26 Query Match Best Local S Matches 226 GENERAL INFORMATION: ZIP: 02173 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: SYSTEM: PC-DOS/MS-DOS COPPRAPING SYSTEM: PC-DOS/MS-DOS APPLICANT: Shen, Xiaoyu APPLICANT: Houman, Fariba TITLE OF INVENTION: CANDIDA CYTOPLASMIC TRYPTOPHANYL-trna TITLE OF INVENTION: SYNTHETASE PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING TITLE OF INVENTION: SAME NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS: TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive LENGTH: 424 amino acids TYPE: amino acid Lexington : MA USA 54.3%; Score 1218.5; DB 4 57.1%; Pred. No. 6.1e-127; tive 71; Mismatches 92; DB 4; Length 424;

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31 TEAEEDFVDPWTVQ----TSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLR 86

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Gaps

TEESEQKITPWEVEGAVVDGKSMGIDYDKLISQFGTKHITEETLERFKQVTGEEPHPFLK 72

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Patent No. 6046174
GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gentry, Danile
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6046174el trpS
                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,100
                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                           STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                 TYPE:
                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                           amino acid
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                                                                                                                                                 341 amino acids
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                                                                                            linear
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                                                                       protein
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8.3%;
24.0%;
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Score 185.5; DB 3; Pred. No. 5.4e-12;
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                   Length 341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gentry
                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                         NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12-SEP-
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                FILING DATE: 12-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
TOPOLOGY: 1
                                 STRANDEDNESS:
                                                  TYPE: amino acid
                                                                                                                                          TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: King of Prussia
                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 DYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 GDAVEN-----AKDIIACGFDINKTFIF--SDLDYMGMSSGFYKNVV---KIQK 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 TDHAKDPOTIVESIGNVALDYLAVGLDPNKSTIFIOSOIPELAELSMYYMNLVSLARLER 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19406-0939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSKS-LNNGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDAQEIADMKE
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                                                                 341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenwood, Claire
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gentry, Danile
              ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                       12-SEP-1997
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 6346409el trpS
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Road
                                                                                                        ν.
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                                                                                                                                                                                                  P31624-1
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Indels Length 341;

69;

Gaps

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----VPVGTDQK 156

371 212

268

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RESULT 4
US-09-425-666-2
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                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P310
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425.666
FILING DATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6416976el trpS
                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                LENGTH:
TYPE: a
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CTTY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                   TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
STRANDEDNESS:
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5. 6416976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDDDKLEQIRK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSKS-LNNGIY 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVTFNQVKGIFGFTDSDCIGKISFPAIQAA--PSFSNSFPQIFRDRTDIQCLIPCAIDQD 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPIIL-TGDRPTGK-LHIGHYVGSLKNR------VLLQEEDKYDMFVFLADQQAL 49
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mino acid
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709 Swedeland Road
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24.0%; Pred. No. 5.4e-12;
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US-09-425-666-2
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Patent No.
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                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/743,130,
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                         REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDII
TITLE OF INVENTION: PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
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                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKY-LWKDLTLDQAY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50
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5871987
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYORGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYTSGAMLTGELKKALIEVLOPLIAEHQARRKEVTDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDAQEIADMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDDDKLEQIRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPTVKTEISOKGFGESIPTGFLVYPIAQAADITAFKANY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPIIL-TGDRPTGK-LHIGHYVGSLKNR------VLLQEEDKYDMFVFLADQQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE - - RAGRLPGLDG - NAKMSKS - LNNGIY
                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
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                                                      (617)
                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tao, Nianjun
Tao, Jianshi
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Gallant, Paul
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                                                                                                                                                                                                                                                                            Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mandana
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                                                                                                                   CPI95-12
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Pred. No. 5.4e-12;
                                                                                                                                                                                                                                                                              Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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RESULT 6
US-08-743-130A-2
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                                                                                                       SOPTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      ATTORNEY/AGENT INFORMATION:
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CANDIDA TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                         FILING DATE: 0: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: li
               REFERENCE/DOCKET NUMBER: CP:
                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 -----EEFQVAQK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 ---PLSY-----DSIEQLKADFVDGKLAPPDLKSGVADKINELLAPIRAEFESS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 CDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALI----EVLQPLIAEHQARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 EEPKVVKKKVNSAYCAPGELKDNGLIAFIEYVIQPIAELKTGVEĞAFKLDIDRPEKYGĞ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VDAQFG-GVDQRKIFVLAEENLPSIGYKKRAHLMNPMVPGL-GQGGKMSASDPNSKIDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 IQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 NVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGF 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2, Application US/08743130A
5. 5871987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 VLDAYENK-KPFYLYTGRGPSSEAMHVGHLIPFI-----FTKWLQDV-----F 140
                                                                                                                                                                                                                                                               02173
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                                                                                                                                                                                                                                                                                                                    Lexington
                                                  Brook Esq., David E.
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                                                                                                                                                                                                                                                                                                Massachusetts
                                                                                                                                                                                                                                                                                                                                     Two Militia Drive
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                                                                                                                                                                                                                                                                                 USA
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Tao, Jianshi
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                                                                                                                                                                                                                                                                                                                                                     Hamilton, Brook,
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                                                                                                                                                                                                                                                                                                                                                                                                              CANDIDA TYROSYL-tRNA SYNTHETASE
PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING
                                                                                                                                                                                                                                                                                                                                                                                              41
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                   CPI95-12
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Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                       Smith & Reynolds, P.C
                                                                                                                                                                Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 409;
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,

APPLICATION NUMBER: FILING DATE: Filed

Filed Herewith

US/08/705,868

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESQ Version 1.5
CURRENT APPLICATION DATA:

COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

COUNTRY: STATE:

U.S.

94304

CITY: Palo Alto

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STREET:

ADDRESSEE:

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                                                                                                                                                                                          Sequence 4, Application US/08705868 Patent No. 5885798
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Best Local Similarity
                                                                                                                                                                          GENERAL INFORMATION:
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                                    CORRESPONDENCE ADDRESS
                                                                         APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING
                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                     KEVTDEIVKEFMTPRK 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEPKVVKKKVNSAYCAPGELKDNGLIAFIEYVIQPIAELKTGVEGAFKLDIDRPEKYGG-
B: Incyte Pharmaceuticals,
3174 Porter Drive
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                                                                                                                                 Bandman, Olga
Coleman, Roger
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                                                                                                                                                                                                                                                                                                              ----EEFQVAQK 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 162.5; DB 2
20.7%; Pred. No. 2.7e-09;
                                                                                                                                                    Olga
                                                                                                                                                                                                                                                                                                                                                                                           ----DSIEQLKADFVDGKLAPPDLKLGVADKINELLAPIRAEFESS-
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                                                                               CYTOKINE
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RESULT 8
US-09-123-615-4
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09123615 Patent No. 6090377
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APPLICANT: Bandman
APPLICANT: Coleman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1184699
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                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
                                                                                                                                                                                                                                     APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                   OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 80; Conserv
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                                                       COMPUTER:
                                                                                                                              COUNTRY:
                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QARRKEVTDEIVKEFMTP--RKLS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDEKWGGN-----KTYTAYVD-----LEKDFAAEVVHPGDLKNSVEVALNKLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SKMSSSEEESKIDLLDRKEDVKKKLKK-AFCEPGNVENNGVLSFIKHVLFPLKSEFVIL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTKMSASDPNSSIFLTDTAKQIKTKVNKHAF-----SGGRDTIEEH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKLKFIKGTDYQLSKEYTLDVYRLSSVVTQHDSKKAGAEVVKQVEHPLLSGLLYPGLQA- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMSKIADFLKAGCEV--TILFADLHAYLDNMKAPWELLELRVSYYENVIKAMLESIGVPL 112
                                                                                                                                                 CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 amino acids
                                                                                                                                                                                     3174 Porter Drive
                                                                                                                            U.S.
                                                                                                                                                                                                                                                                                                                Bandman, Olga
Coleman, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 132.5; DB 2 clarity 20.8%; Pred. No. 5.3e-06; Conservative 58; Mismatches 121
                                            3: Diskette
IBM Compatible
                                                                                                                                                                                                     Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DPIREKFNTPALKKLA 337
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RESULT 9
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                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                    Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%; Score 132.5; DB 3; Best Local Similarity 20.8%; Pred. No. 5.3e-06; Matches 80; Conservative 58; Mismatches 121;
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 1184699
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0117 US
                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
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TYPE: amino acid
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                                                                                                                                                                                                                                                               1, Application US/08855910 6221640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGA 299
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Gallant, Paul L.
Shen, Xiaoyu
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                                                                                Avruch, Anthony S. Yu, Russell V. Nair, Shamila
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                                       ENTEROCOCCAL AMINOACYL-tRNA SYNTHETASE PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
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                                                                                                                                                      US-09-352-990-28
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                                                                                                                Sequence 28, Application US/09352990 Patent No. 6255090
                                                                                             GENERAL INFORMATION:
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          APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,910
FILLING DATE: 14-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
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REFERENCE: BB-1191
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                                                                                                                                                                                                                                    327 DLTIEEIEQGLEHVPTV-EITKDAKNIVDWLVDTEIEPSK 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 GPEAKVFGLTIPLMLKADGTKFGKTAGGAIWLDPKKTSPFEFYQFWLNQDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 CGFDINKTFIFSDLDYMGMSS-GFYKNVVKIQKHVTFNQVKG------
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Two Militia Drive
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CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,866
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
SEQ ID NO 28
LENGTH: 377
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2,
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                                                                                                                                                                         ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
                                                                                                                                                                                                                                                   STATE:
APPLICATION NUMBER: 9619 FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                                                 CITY: King of Prussia
                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                       FILING DATE:
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 L-LHSTFFPALQGAQTKMSASDPN--SSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQF 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 DEKYLWKDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 FSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 DNFFCVVDLHAITVPHNPQTLAQ----DTLTIAALYLACGIDLQYSTIFVQSHVAAHSELA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 FAHRSTTAM-----DKPRIL-SGVQPTGN-LHLGNYLGAI-RSWVEQ------QQHY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
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5851809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNSFPQIFRDRTDIQCL----IPCAIDQDPYFRMTRDV------APRIGYPKPA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----IEVLOPLIAEHQARRKEVTDEIVK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRKEGARVMSLADGTKKMSKSDESELSRINLLDPPEMIKKKVKK-
                                                                                                                                                                                                                                                   PA
                                                                                                                                                                                                                                                                                    E: SmithKline
709 Swedeland
                                                                                                                                                                                                                                                                                                                                                      Lawlor, Elizabeth
                                                                                                                                                                                                                                  USA
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                                                                  04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DILLYDADKVEVGEDOKQHLELTRDIVIRINDKFGREDAFVLKLPEPL
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21.0%; Pred. No. 0.0021;
                  9619072.3
                                                                                        US/08/923,867
                                                                                                                                                                                                                                                                                      Beecham Corporation Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478

REFERENCE/DOCKET NUMBER: NAME: Gimmi, Edward REGISTRATION NUMBER:

Gimmi,

Edward R

38,891

P31624

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RESULT 12
US-08-928-100-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08928100 Patent No. 6046174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                            APPLICATION NUMBER: US/08/928
FILING DATE: 12-SEP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                           REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 709 STREET CITY: King of Prussia
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                                                 TELEFAX:
                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                TELEX:
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TLE OF INVENTION: No. 6046174el trpS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                                                                                                                                                                                                                                    19406-0939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-LNNGIYLADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPVGTDQKPMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSK 61
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                                                610-270-5090
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                                                                 610-270-4478
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25.3%; Pred. No.
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73;
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                                                                      US-09-183-134-2
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Best Local Similarity 25.3
Conservative
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Patent No. 6165759
                                  Query Match
                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: NOVEL TRYPTOPHANYL tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 9619072.3
APPLICATION NUMBER: 9619072.3
TITMIT DATE: 12-SEP-1996
Local Similarity 25.3%; Pr
                                                                                                                                                                                                                                                                             NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                        TOPOLOGY: linear
                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                              TELEFAX: 610-270-5090
                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 QEIADMKERYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 DKLEQIRKDYTSGAMLTGELKKALIEVLOPLIAEHQARRKEVTDEI 409
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                                                                                                                                     amino acid
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                                                                                                                                                     197 amino acids
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25.3%; Pred. No. 0.00092;
ive 27; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                    08/923,867
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                                                                                                                                                                                                                                                                                           38,891
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                                                                                                                                                                                                                                                                                P31624
                                  DB 4; Length 197;
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                                                                                                                                        Matches
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                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atent No. 6346409
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/928,100
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-1996
ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                                                                TOPOLOGY: 1i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                   TYPE: amino acid
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REFERENCE/DOCKET NUMBER:
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ZIP: 19406-0939
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                               306 SDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSPMYLTFF--LEDD 363
                                                                                                      260 IPCAIDODPYFRMTRD-------VAPRIGYPKPALLHSTFFPALQGAQTKMSA 305
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62 S-LNNGIYLADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDA 116
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42; Conserv
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709 Swedeland Road
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Lawlor, Elizabeth
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Pred. No. 0.00092;
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US-09-425-666-4
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US-09-425-666-4
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Best Local
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NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P316
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS LENGTH: 197 amino acid
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 610-270-5090
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117
                                                                                         306 SDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDD 363
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                              364 DKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 409
                                                                                                                                                     260 IPCAIDODPYFRMTRD-----
                                                            62 S-LNNGIYLADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDA 116
                                                                                                                      5 VPVGTDQKPMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSK 61
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QEIADMKERYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 162
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    SmithKline Beecham Corporation
709 Swedeland Road

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Search completed: July 10, 2003, 12:32:50 Job time : 15.8485 secs

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Result
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Perfect score:
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 Pred. No.
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re greater than or equal to the score of the result being prints
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Gapop 10.0 ,
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	YWBSF	S73024	E82052	C72370	H69102	AI1066	F71093	臣64676	T03741	C84374	C72034	H86590	T44994	C81654	B75072	F71300
	tryptophan-tRNA li	tryptophan-tRNA li	tryptophanyl-tRNA	tryptophan-tRNA li	tyrosine-tRNA liga	tryptophan-tRNA li	tyrosine-tRNA liga	tryptophan-tRNA li	probable tyrosine-	tyrosyl-tRNA synth	tryptophan-tRNA li	tryptophanyl tRNA	probable tryptopha	tryptophanyl-tRNA	tyrosyl-tRNA synth	tryptophan-tRNA li

ALIGNMENTS

A:Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response elemen	nt onha
Gene 128, 237-245, 1993	-trna
R;Frolova, L.Y.; Grigorieva, A.Y.; Sudomoina, M.A.; Kisselev, L.L.	RNA li
A;Note: 213-Ser and 214-Tyr were also found	RNA li
A;Cross-references: EMBL:X62570; NID:g32708; PIDN:CAA44450.1; PID:g32709	RNA li
A;Residues: 1-423,'R',425-471 <buw></buw>	-tRNA
A; Molecule type: mRNA	RNA li
A;Status: preliminary	-tRNA
A;Accession: S19246	-tRNA
A;Reference number: S19246; MUID:92164636; PMID:1537332	RNA li
A; Title: Molecular cloning and characterization of an interferon induced human cDNA with	prote
EMBO J. 11, 489-496, 1992	RNA li
R;Buwitt, U.; Flohr, T.; Boettger, E.C.	RNA li
A;Cross-references: GB:M77804; NID:g184656; PIDN:AAA67324.1; PID:g184657	RNA li
A;Residues: 1-471 <rub></rub>	RNA li
A; Molecule type: mRNA	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
A;Status: preliminary	
A;Accession: A41706	
A;Reference number: A41706; MUID:92105071; PMID:1761529	
A;Title: Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts.	
J. Biol. Chem. 266, 24245-24248, 1991	
R;Rubin, B.Y.; Anderson, S.L.; Xing, L.; Powell, R.J.; Tate, W.P.	
A,Cross-references: GB:X59892; NID:g30820; PIDN:CAA42545.1; PID:g30821	ited,
A; Residues: 1-471 < FLE>	
A; Molecule type: mRNA	-
A;Status: preliminary	
A;Accession: A41633	
A; Reference number: A41633; MUID: 92107982; PMID: 1763065	
A.Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamma	
Proc. Natl. Acad. Sci. U.S.A. 88, 11520-11534, 1991	
D.F. ocknor J. Dagmicgon H. H. Jigtesen J	
C:Accession: A41633: A41706: S19246: JN0676: JH0533: S26287	
C.Jate. 10-May. 2000 #agnience revision 10-May. 2000 #text change 03-Jun-2002	
N;Alternate names: interferon-inducible protein IFP53; peptide-chain release factor homol	
tryotophan-tRNA ligase (EC 6.1.1.2) [similarity] - human	
RESULI L	

A,Molecule type: DNA
A,Residues: 1-141;182-471 <FRO1>
A,Residues: 1-141;182-471 <FRO1>
A,Cross-references: GB:X67918; GB:S62855; NID:g37975; GB:X67926; GB:X67926; NID:g37976; GB:X67926; A; NID:g37974; GB:X67925; GB:S62855; NID:g37976; GB:X67926; GB:X67926; MID:g37976; GB:X67926; A; Note: the authors translated the codon GGG for residue 55 as Cys and GAG for residue 34 A; Note: this translation is not annotated in GenBank entries HSWRSXIA, HSWRSXIB, HSWRSX2, R; Frolova, L.Y.; Sudomoina, M.A.; Grigorieva, A.Y.; Zinovieva, O.L.; Kisselev, L.L.
Gene 109, 291-296, 1991
A;Title: Cloning and nucleotide sequence of the structural gene encoding for human trypto A; Reference number: JH0533; MUID:92112058; PMID:1765274

A;Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response elemer A;Reference number: JN0676; MUID:93292992; PMID:7685728 A;Accession: JN0676

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tryptophan-tRNA ligase (EC 6.1.1.2) [validated] - bovine
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 03-Jun-2002
C;Accession: A40279; JN0354; S10460; S14540
R;Garret, M.; Pajot, B.; Trezeguet, V.; Labouesse, J.; Merle, M.; Gandar, J.C.; Benedett Biochemistry 30, 7803-7817, 1991
A;Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic ship. Accession: A40279; MUID:91329348; PMID:1907847
A;Accession: JM0354; MUID:91329348; PMID:1907847
A;Accession: JM0354
A;Molecule type: protein
A;Accession: JM0354
A;Molecule type: protein
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A;Cross-references: GB:M61715; NID:g340367; PIDN:AAA61298.1; PID:g340368
A;Experimental source:,fibroblast
C;Genetics:
A;Gene: GB:WARS; IFP53
A;Gross-references; GDB:119632; OMIM:191050
A;Map position: 14q23-14q31
A;Map position: 14q23-14q31
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase r
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis F;19-64/Domain: amino acid-tRNA ligase repeat homology <ATL>
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tryptophan-tRNA ligase (EC 6.1.1.2) [validated] - rabbit N,Alternate names: tryptophanyl-tRNA synthetase C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 30-Sep-1992 #sequence revision 13-Feb-1998 #text_chan C;Accession: A35904; 837396  
C;Accession: A35904; 837396  
R;Lee, C.C.; Craigen, W.J.; Muzny, D.M.; Harlow, E.; Caskey, Proc. Natl. Acad. Sci. U.S.A. 87, 3508-3512, 1990 A;Title: Cloning and expression of a mammalian peptide chain A;Reference number: A35904; MUID:90239043; PMID:2185472
A;Gene: WRS
C;Complex: homodimer [validated, MUID:94009008]
C;Function:
C;Function: EC 6.1.1.2 [validated, MUID:94009008];
A;Note: mammalian WRS (tryptophanyl-tRNA synthetases)
C;Superfamily: mammalian tryptophan-tRNA ligase; amino
                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-475 <LEEA
A;Cross-references: GB:M33460
R;Frolova, L.Y.; Dalphin, M.E.; Justesen, J.; Powell, R.
EMBO J. 12, 4013-4019, 1993
A;Title: Mammalian polypeptide chain release factor and
A;Reference number: S37396; MUID:94009008; PMID:8404867
A;Accession: S37396
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C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence revision 10-Nov-1995 #
C;Accession: S50053; S50052; T49391; S31461; S31462
R;Pajot, B.; Sarger, C.; Bonnet, J.; Garret, M.
J. Mol. Biol. 242, 599-603, 1994
                                                                        A,Title: Mammalian tryptophanyl-tRNA synthetases.
A;Reference number: I49391; MUID:94257729; PMID:7515282
A;Accession: I49391
                                                                                                                                                                                                                                                                                                         A;Title: An alternative splicing modifies the C-terminal end A;Reference number: S50052; MUID:95018226; PMID:7932716 A;Accession: S50053
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A;Cross-references: EMBL:X69657; NID:g55437; PIDN:CAA49348.1; PID:g55438 C;Genetics: <LSF>
                              A; Residues: 1-481 < RES>
                                          A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                    Biochimie 75, 1027-1039, 1993
                                                                                                                                 A;Genetics: SSF
R;Kisselev, L.L.
                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-475 <PAW>
A;Cross-references: EMBL:X69656;
                                                                                                                                                                                                                A;Note: intron position was determined A;Accession: S50052
                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-481 < PAJ >
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                                                                                                                                                                                                                                                  Genetics: LSF;
                                                                                                                                                                                                                                                               Cross-references:
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ilarity 89.8%;
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C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology C;Keywords: alternative splicing; aminoacyl-tRNA synthetase; ligase; protein biosynthesis F;1-481/Product: tryptophan-tRNA ligase alpha-2 chain long splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;23-68/Domain: amino acid-tRNA ligase repeat homology <ATL>
                     A; Experimental source: strain C; Genetics:
                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-395 <GE2>
A;Cross-references: EMBL:Z50142; PIDN:CAA90500.1; GSPDB:GN00066;
A;Experimental source: strain 972h-; cosmid c2F7
                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein SPAC2F7.13c - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 10-Dec-1999 C;Accession: S58157; T38561 R;Gentles, S.; Churcher, C.M.
                                                                                                                                                         A; Reference number: Z21799
A; Accession: T38561
                                                                                                                                                                                                    A;Cross-references: EMBL: 250142; NID: 91052783; PIDN: CAA90500.1; R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                       R;Gentles, S.; Churcher, C.M. submitted to the EMBL Data Library,
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A;Note: the list of introns
C;Genetics: <SSF>
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A, Accession: S58157
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A; Residues: 1-395 <GEN>
                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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Pred. No. 2.8e-157;
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Walsh, S.V.
                                                                     SPDB:SPAC2F7.13c
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A;Residues: 1
A;Cross-refe;
A;Experimenta
C;Genetics:
A;Gene: SGD:V
                                                                                                                                                                                     A, Reference number: S59156; MUID:96076631; PMID:7502582
A; Accession: S59177
A; Status: nucleic acid sequence not shown; translation not show A; Molecule type: DNA
A; Residues: 1-432 < VAW-
A; Cross references: EMBL:Z48149; NID:g663234; PIDN:CAA88164.1; A; Note: the nucleotide sequence was submitted to the EMBL Data R; Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M. submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tryptophan-tRNA ligase (EC 6.1.1.2) [similarity] - yeast (Saccharomyces cerevisiae) N;Alternate names: protein HRE432; protein 00792; tryptophanyl-tRNA synthetase C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 05-May-1995 #sequence revision 03-Aug-1995 #text_change 03-Jun-2002 C;Accession: S51901; S59177; S66793 C;Accession: S51901; S59177; Portetelle, D.; Hilger, F.
                                                            A;Accession: S66793
A;Molecule type: DNA
A;Residues: 1-432 <DUR>
A;Cross-references: EMBL:Z74839; NID:g1419947; PIDN:CAA99110.1; PID:g1419948; GSPDB:GNO
                                                                                                                                                                                                                                                                                                                                                                                                           R;Vandenbol, M.; Durand, I
Yeast 11, 1069-1075, 1995
A;Title: Sequence analysis
a delta element.
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C; Superfamily: may
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A; Residues: 1-432 < VAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, January 1995
A;Description: Sequence analysis of a 44kb DNA f
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                                                                                                                                                                      A; Reference number: S66791
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                                               Experimental source: strain
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Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
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Best Local Similarity
Matches 235; Conserv
SGD:WRS1; WRS1; MIPS:YOL097c
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence analysis of a 44 kb DNA fragment of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 KLÍQOFVSDFQAARSKVDEATLDMFMDGSRKLEW 395
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59.6%; Pred. No. 1.5e-90;
tive 60; Mismatches 91;
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A;Cross-references: SGD:S0005457
A;Map position: 15L
C;Superfamily: mammalian tryptophan-tRNA ligase;
C;Keywords: ligase
F;117-120/Region: ATP-binding motif (HXGH)
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Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryptophanyl-tRNA synthetase (trpS) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001 C;Accession: C90190
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C;Genetics:
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A; Residues: 1-386 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 VIQMTDDEKYLMK-DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 203
                                                                                                                                                 31 TEABEDFVDPWTVQTSSAKG-IDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
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217; Conserv
                                                                         90 FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMT 149
                                                                                                                                                                                                                   Similarity
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                                                                                                                  TMPDEFTVTPWEV-----KGKVDYDKLIVQFGTQKITEELKQRIKNLAGDL-HVMLRRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKALIEVLOPLIAEHOARRKEVTDEIVKEFMTPRKL 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRKGLFFSERDFTKILDLYEQGKPFFLYTGRGPSSDSMHLGHMIPFVFTKWLQEVFDVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STDVKEQVVTPWDVEGGVDEQGRAQNIDYDKLIKQFGTKPVNEETLKRFKQVTGREPHHF
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                                         FFSHRDLDLVLNDYEKSKGFFLYTGRAPSL-GMHIGHLIPFIFTKWLQEKFNANLYIEIT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKLCIETLQEFVKAFQERRAQVDEETLDKFMVPHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KINKYÁFSGGQVSADLHRELGGNPDVDVAYQYLSFFKDDDVFLKECYDKYKSGELLSGEM
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                                                                                                                                                                                                                                                                            mammalian
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                   40.4%; Score 907; DB 2;
48.6%; Pred. No. 6.2e-66;
                                                                                                                                                                                                                                                                          tryptophan-tRNA ligase; amino acid-tRNA
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Pred. No. 1.1e-86;
1; Mismatches 100
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome
                                                                                                                                                                                                   110;
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goc, H.P.;
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C;Superfamily: mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50601.1; PID:g54591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-385 < KAW >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: C75020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: R; anonymous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tryptophanyl-tRNA synthetase (trps)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Pyrococcus abyssi
Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
342
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                                                                                                                                                                                                                          213
                                                                                                                                                                                                                                                                                     154 YLWKD-LTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVT 212
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                                                                                                                                                                                                                                                                                                                                       RDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEK 153
KIQEFLKEHQKRRKKAEKQIEK 363
                                                                                                                            QRDFAESLGYYKTAAIHSKFVPSLTSLSGKMSASKPETAIYLTDSPEDVEKKVWKFALTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDD-KLEQIRKDYTSGAMLTGELKKAL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLQPLIAEHQARRKEVTDEIVK 411
                                                                                                                                                          TRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSG
                                                                                                                                                                                                                                                          FLFKENLTFEDTKHWÄYENILDIIAVGFDPDKTFIFQNSEF----TKIYEMAIPIAKKIN 173
                                                                                                                                                                                                                                                                                                                        RDYDKVLQDYEEGRGFFLYTGRGPSG-PMHIGHIIPFFATKWLQEKFGVNLYIQITDDEK 117
                                                                                                                                                                                                                                                                                                                                                                                        EDFKVTPWEVEGV-----VDYNKLIEHFGTSPLTEELLEKTAELTKSELPLFFRRKFFFSH
                                                                                                                                                                                                                                                                                                                                                                                                                    EDF-VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDKLNNFLEEHR-RREEAKELVHVFKYDGKLA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEVLOPLIAEHOARRKEVTDEIVKEFMTPRKLS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFSGGQPTIELHRKYGGNPEIDVPFQWLYYFFEEDDNRIKEIEEEYRSGKMLTGELKQIL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YWRLQRDIAESLGYYKAAQIHSKFLPPLTGPEGKMSSSNPETAIYLVDDPKTVERKIMKY
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                                                               ĠŔPTLKEQŔEKĠĠEPEKCŶVFKWĹEIFFÉEDDŔ--KLKERYYACKNĠELTCĠECKRYĹÍS 341
                                                                                          GRDTIEEHROFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 389
                                                                                                                                                                                            FSMAKAVFGFTEQSKIGMIFFPAIQIAPTF----FEKR---RCLIPAAIDQDPYWRL
                                                                                                                                                                                                                        FNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRM 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 803; DB 2;
Pred. No. 1.8e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 385
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                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <STO>
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Best Local (
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                                                                                                                                                                                                                                                                                                                                         KLA 286
                                                                                                                                                                                                                                                                                                                                                                       KLS 420
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C;Accession: G84373
C;Accession: G84373
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lian, J. J.; Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tryptophan-tRNA ligase (EC 6.1.1.2) - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 03-Jun-2002
A;Cross-references: GB:AE004437; NID:g10581646; PIDN:AAG20355.1; GSPDB:GN00138 C;Genetics: A;Gene: tryS2 A;Gene: tryS2 C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
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DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome
A;Title: Complete sequence and gene organization of the genome
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C;Keywords: aminoacyl-tRNA synthetase; ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tryptophanyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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A;Experimental source: strain OT3
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M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 MHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKD-LTLDQAYGDAVENAKDIIACGF
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44.2%; Pred. No. 2.86
tive 56; Mismatches
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J.; Kushida,
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A; Status preliminary; nucleic acid sequence not shown; translation not A; Residues: 1-370 <BUL>
A; Residues: 1-370 <BUL>
A; Cross-references: GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99425.1; C; Genetics:
A; Map position: FOR1375885-1376997
A; Map position: FOR1375885-1376997
A; Start codon: GTG
C; Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase C; Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tryptophan-tRNA ligase (EC 6.1.1.2) - Methanococcus jannaschii
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Jun-2002
C;Accession: F64476
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bla); Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Renc, T. Colon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannass
A;Reference number: A64300; MUID:96337999; PMID:8688087
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Best Local Sim:
Matches 141;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 119; Conserv
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                                                                                                       100 LDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQ---DVFNVPLVIQMTDDEKYLW 156
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               KDLTLDQAYGDAV-ENAKDIJACGFDINKTFIFSDLDYMGMSSGFYKNVVKI-QKHVTFN
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                                                              VDAIKNNKEFAVVSGMMPSGK-MHFGHKMVVDLLKFYQKYTDNINIPI----ADLEAYWA
                                                                                                                                                    PW--ETPAV--IDYKKTMEQFGVKPIVDVLGDLKEE-----
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30.9%; Pre
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                                                                                                                                                                                                                                                           Score 409.5; DB 2
Pred. No. 1.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 534.5; DB 2;
Pred. No. 1.2e-35;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VTEALDAFRLTDD
                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                             Length 370;
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                                                                                                                                                    -HHFFRRNIILGHRDFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN: AAB99425.1; PID: g1592065;
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dek, A.
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A; Start codon: 'C; Superfamily: I
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A; Status: preliminary.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J.; Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec:1997 #sequence_revision 05-Dec:1997 #text_change
C;Accession: E69131
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A; Residues: 1-364 < MTH >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keywords:
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                                                                                                                                                                                                                                                                                                                                              158 DLTLDQAYGDAVEN-AKDIIACGFDINK-----TFIFSDLDYMGMSSGFYKNVVK 206
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                                                                                                                                                                                                                                                                                                                                                                                         51 RIISAMKKGEDFAVVTGMMPSGR-MHIGHKMIVDQLRW-YDRMGAEIFIPIADMEAYSAR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                    98 QVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ly: mammalian tryptophan-tRNA ligase; amino aminoacyl-tRNA synthetase; ligase; protein
                                                                                   TKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLE-DDDKLEQIRKDYTSGAMLTG
                                                                                                                                                                 DPYFRMTRDVAPRI----GYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIK 322
                                                                                                                                                                                                                                                         IQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQ
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ELKKALIEVLQPLIAEHQARRKE 404
                                          AKI-RNAKTGGRETLKEQRELGGVPEECIIYETLLYHMSGSDSRLEEIYESCRNGTLMCG
                                                                                                                                DPHIRLTRDIAARFRDRYGFILPSSTYHRFMGGLTGG--KMSSNRPKSAIFLSDTPEEAE
                                                                                                                                                                                                                   LAGKVNFNELRAIYGFTGSTSMAHMYAPIIQVSDILHPQLDELGGPR----PVIVPVGPDQ
                                                                                                                                                                                                                                                                                                      GVDFEDSRRIAIEEYIAGYIALGLDLEKDNIHVYLQSENLMVEDLAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDPW----GSAK-LEYODLIENFGVRPF-SEVLDEV-----PEPSWLMRRGIIFGHRDYE 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%; Score 397.5; DB 2 27.9%; Pred. No. 1.6e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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biosynthesis
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cryptophanyl-tRNA synthetase (trpS) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: B69461
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Beference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AJ012470; PIDN:CAA10034.1
C;Superfamily: mammalian tryptophan-tRNA ligase; ar
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Peyretaillade, E.; Broussolle, V.; Peyret, P.; Metenier, Mol. Biol. Evol. 15, 683-689, 1998
A;Title: Microsporidia, amitochondrial protists, possess a A;Reference number: 222693; MUID:98277683; PMID:9615449
A;Accession: T43806
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tryptophan-tRNA ligase (EC 6.1.1.2) [imported] - Encephalitozoon cuniculi (fragment) C;Species: Encephalitozoon cuniculi (fragment) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 03-Jun-2002 C;Accession: T43806
                                                                              8
                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-420 <KLE>
A;Cross-references: GB:AE000986; GB:AE000782; NID:g2689309; PIDN:AAB89554.1; PID:g26488:
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
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                                                                                                                                                                VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAHRDFNLLLDEIANNRPFYLYTGRGPSSKTMHIGHTIPFLLCKYMQDAFKIRLVIQITD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDFVDPWTVQTSSAK----GIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIF 90
DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVV-KIQKHVTFNQV 216
                                        RIIEAMQKKEPWAVMSGFMPSG-LPHFGHKMTMDEIVWHQSAGGKAFV-AIADMEAHSVR
                                                                                   QVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWK 157
                                                                                                                                VTPWEVEGV----IDYSKLIEEFGMQPF-SEVLPEID-----NPHILMRRGAIFGHRDYW 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEKFLWKSMRLE 134
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                 16.5%; Score 370.5; DB 2; 27.3%; Pred. No. 3e-22; tive 60; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.2%; Score 386; DB 2; Length 134. 51.5%; Pred. No. 3.2e-24; tive 25; Mismatches 35; Indels
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probable tryptophanyl-tRNA synthetase APE2461 - Aeropyrum pernix (strain K1. C;Species: Aeropyrum pernix (C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 C;Accession: D72477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: APE2461
C;Superfamily: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81476.1; A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A72450; A; Accession: D72477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complete genome sequence of an aerobic hyper-thermophilic A;Reference number: A72450; MUID:99310339; PMID:10382966
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                                                   FSGGRDTIEEHRQFGGNCDV-DVSFMYLTFFLEDDDKLEQIRKDYTS---GAMLTGELKK 385
                                                                                                                                                            RDVAPR----IGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHA 329
                                                                                                                                                                                                                     EMEATYGELTPAKMMASLT----QAADILHVQLDEYGGYR---HVVVPVGADQDPHLRLT
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LTGGRATAEEQRRLGGVPEVCSVYHMDLYHLMPDDGEVKHI---YTSCRLGKILCGECKQ
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Qy 386 ALIEVLQPLIAEHQARRKEVTDEIVKEFMTPR 417

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Db 342 IAWEKLERFLAEHQSRLEKAKTIAWKLVEPPR 373

Search completed: July 10, 2003, 12:32:17

Job time: 18.4461 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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P23612 oryctolagus
P32921 mus musculu
Q09692 schizosacch
Q12109 saccharomyc
  P32922
Q09292
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EMBL; M77804; AAA67324.1; -
EMBL; K59892; CAA42545.1; -
EMBL; K62570; CAA44450.1; -
EMBL; S82905; AAB39381.1; -
EMBL; S82905; AAB39381.1; -
EMBL; K67920; CAB94198.1; J
EMBL; K67921; CAB94198.1; J
EMBL; K67922; CAB94199.1; J
EMBL; K67923; CAB94199.1; J
EMBL; K67924; CAB94199.1; J
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EMBL; K67928; CAB94199.1; J
              CONFLICT
                                                                                                         PROSITE;
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Pfam; PF00579; tRNA-synt 1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tryptophanyl-tRNA synthetase.";
FEBS Lett. 300:162-166(1992).
-I-CATALYTIC ACTIVITY: ATP + L-tryptophan +
diphosphate + L-tryptophanyl-tRNA(Trp).
-I- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frolova L.Y., Grigorieva A.Y., Sudomoina M.A., Kisselev L.L.; "The human gene encoding tryptophanyl-tRNA synthetase: interf response elements and exon-intron organization."; Gene 128:237-245(1993).
                                                                                                                                                                                                                                                                 Genew; HGNC:
MIM; 191050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
                                                                          DOMAIN
                                                                                                                                                                                                                                                                                              Aarhus/Ghent-2DPAGE;
PHCI-2DPAGE; P23381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bange F.-C., Flohr T., Buwitt U., Boettger I "An interferon-induced protein with release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rasmussen H.H., van Damme
Vandekerckhove J.;
                                                                                         Aminoacyl-tRNA
                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92225128; PubMed=1373391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Microsequences of 145 proteins recorded in protein database of normal human epidermal k Electrophoresis 13:960-969(1992).
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INDUCTION: BY INTERFERON GAMMA.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE
SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
                                                                                                                                                                                                                                                                               HGNC:12729; WARS.
                                                                                                                                                                                              IPRO02306; Trp tRNA-synt 1b.
IPRO00738; WHEP-TRS.
IPRO02305; tRNA-synt 1b.
IPRO01412; tRNA-synt I.
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           WHEP-TRS.
"HIGH" REGION.
"KMSKS" REGION.
SY -> GD (IN RE
A -> R (IN REF.
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R (IN REF. 4).
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P17248;
01-AUG-1990
01-MAY-1992
15-JUN-2002
                                                                                                                                                                                                                                                                                                       U1-AUG-1990 (Rel. 15, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (TryRS).
           Garret M., Trezeguet V., Pajot
Guegueiv M., Benedetto J.-P.,
Labouesse J., Bonnet J.,
Submitted (MAR-1990) to the EN
                                                                                                           "A mammalian tryptophanyl-tRNA synthetase shows little homology prokaryotic synthetases but near identity with mammalian peptide chain release factor.";
                                                                                                                                             Garret M., Pajot B., Trezeguet V., Labouesse J., Merle M., Gandar J.-C., Benedetto J.-P., Sallafranque M.-L., Alterio Gueguen M., Sarger C., Labouesse B., Bonnet J.;
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                                                                                                 Biochemistry 30:7809-7817(1991)
                                                                                                                                                                                  MEDLINE=91329348; PubMed=1907847;
                                                                                                                                                                                               SEQUENCE FROM N.A., TISSUE=Retina;
                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                Bovidae;
                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                        SEQUENCE OF 17-475
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ATP + L-tryptophan + t
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Sarger C., Alteriot
L-tryptophan + tRNA(Trp)
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Query Match
Best Local
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CONFLICT
SEQUENCE
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Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
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InterPro; IPR0002306; Trp tRNA-synt lb.
InterPro; IPR000738; WHEF-TRS.
InterPro; IPR0002305; tRNA-synt lb.
InterPro; IPR001412; tRNA-synt I.
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EMBL; X52113; CAA36356.1; -.
EMBL; A40279; YWBO.
PIR; S14540; S14540.
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DOMALN
24
69
WHEP-TRS.
DOMAIN
1 117
DISPENSABLE TO THE CATALYTIC ACITVITY.
SITE
169
178
"HIGH" REGION.
SITE
353
357
"KMSKS" REGION.
CONFLICT
17
17
L -> M (IN REF. 2).
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PROSITE; PS00178; AA TRNA LIGASE_I; 1.

PROSITE; PS00762; WHEP_TRS; 1.
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SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE
SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
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DFQ 475
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                                                                                DDDKLEQIRRDYTSGAMLTGELKKELIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSY
                                                                                                         DDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSF
                                                                                                                                                                KMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTVEEHRQFGGNCDVDVSFMYLTFFLE
                                                                                                                                                                                            KMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLE
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Pred. No. 6.7e-169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "KMSKS" REGION.
L -> M (IN REF. 2).
F7E531750137EB32 CRC64;
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RESULT

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SSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEA

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SYW_RABIT
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01-NOV-1991 (Rel. 2
15-UUL-1998 (Rel. 3
15-UUL-1998 (Rel. 3
Tryptophanyl-tRNA 6
                                                                                                                                                                                                                                         PRINTS; PRO1039; TRNASYNTHIRP,
TIGRRAMS; TIGRO233; trpS; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
PROSITE; PS00762; MHEP TRS; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; DOMAIN
23 68 WHEP-TRS.
SITE 353 357
SITE 353 357
KMSKS" REGION.
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KMSKS" REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frolova L.Y., Dalphin M.E., Justesen J., Powell R.J., Drugeon McCaughan K.K., Kisselev L.L., Tate W.P., Haemni A.-L.; "Mammalian polypeptide chain release factor and tryptophanyl-t synthetase are distinct proteins."; EMBO J. 12:4013-4019(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR000738; WHEP-TRS.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00458; WHEP-TRS; 1.
Pfam; PF00579; tRNA-synt_lb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M33460; AAA31246.1; ALT_SEQ
EMBL; U02595; AAB60257.1; -.
PIR; A35904; YWBBPR.
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Lee C.C., Craigen W.J., Muzny D.M., Harlow E., Caskey C.T.;
Lee C.C., Craigen W.J., Muzny D.M., Harlow E., Caskey C.T.;
"Cloning and expression of a mammalian peptide chain release factor
with sequence similarity to tryptophanyl-tRNA synthetases.";
with sequence similarity to tryptophanyl-tRNA synthetases.";
proc. Natl. Acad. Sci. U.S.A. 87:3508-3512(1990).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS TO 169-174 AND 227-228, AND FUNCTION MEDLINE=94009008; PubMed=8404867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + L-tryptophan + trua (
diphosphate + L-tryptophanyl-trua(Trp).
SUBUNIT: HOMODIMER (BY SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRUA
SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RABIT
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                                                                                                                               383;
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                                                                                                                                                            Similarity
      SYKEAMGEDYKADCPPGNSTPDSHGDPEAVDDKEDFVDPWTVRTSSAKGIDYDKLIVQFG
                                         SYKAAAGEDYKADCPPGNPAPTSNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFG
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ilarity 90.5%;
Conservative 2
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36, Last sequence update)
36, Last annotation update)
synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                      Score 2056; DB 1;
Pred. No. 2.1e-162;
0; Mismatches 20;
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                                                                                                                                                                                   Length 475;
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SYW_MOUSE
P32921;
01-OCT-1993
                                                                 EMBL; X69656; CAA49347.1;
EMBL; X69657; CAA49348.1;
PIR; S31461; S31461.
PIR; S31462; S31462.
                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AN MEDLINE=95018226; PubMed=7932716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1993
15-JUN-2002
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WARS OR WRS.
MGI:104630; Wars.
rPro; IPR002306; Trp_tRNA-synt_lb.
rPro; IPR000738; WHEP-TRS.
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(Rel.
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. 27, Last sec
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A synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
thetase (EC 6.1.1.2) (Tryptophan--trNA
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Sciurognathi; Muridae;
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; Murinae; Mus
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Best Local
                                                                                                                               SYW_SCHPO STANDARD; PRT; 395 AA.
(006592;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TrypRS).
SPAC2F7.13C.
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SEQUENCE
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InterPro; IPR001412; tRNA-8ynt I.
Pfam; PF00458; wHEP-TRS; 1.
Pfam; PF00579; tRNA-8ynt 1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A.,
                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SITE
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PROSITE; PS00178; AA TRNA LIGASE I;
PROSITE; PS00762; WHEP TRS; 1.
                                         SEQUENCE FROM N.A.
                                                              Schizosaccharomyces.
NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSSKIDKELINRIERATGORPHRFLRRGIFFSHRDMNQILDAYENKKPFYLYTGRGPSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSE
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                                                                                                                                                                                                                                                                                                                FDFQ 424
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168 17
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481 AA;
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357 ":
481 M
54282 MW;
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MISSING (IN ISOFORM; B05A452C08074F52 (
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Pred. No. 2e-160;
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"HIGH" REGION
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CRC64;
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Nicherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Hoodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Giffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415.871.880 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_l.
Pfam; PF00579; tRNA-synt_lb; l.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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i- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
diphosphate + L-tryptophanyl-tRNA(Trp).

i- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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SITE 91 100
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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YFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKH
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                                                                                                          KCITANQSKACFGFTDSDSIGKIHFASIQAAPSFSSSFPHIFNGAKDIPCLIPCAIDQDP
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                                                                                                                                                                                                                                                                                                                       DDEKYLWKD-LTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQ
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Query Match
Best Local Similarity
Matches 217; Conserv
                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z48149; CAA88164.1; -.
EMBL; Z74839; CAA99110.1; -.
SGD; S0005457; WRS1.
InterPro; IPR002306; Trp_trNA-synt_1b.
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00579; tRNA-synt_1b; 1.
PRLNTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WRS1 OR YOL097C OR HRE432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYWC
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Vandenbol M., Durand P., Portetelle D., Hilger F.;
Vandenbol M., Durand P., Portetelle D., Hilger F.;
"Sequence analysis of a 44 kb DNA fragment of yeast chromosome including the Tyl-H3 retrotransposon, the sufl(+) frameshift suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the year transfer RNA-Thr-la and suppressor gene for tRNA-Gly, the year transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la and transfer RNA-Thr-la 
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35,
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                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                      PRINTS; PROJUCT TICRO023; trpS; 1.

PROSITE; PS00178; AA TRNA LIGASE I; 1.

PROSITE; PS00178; AA TRNA LIGASE I; 1.

Aminoacyl-trna synthetase; Protein biosynthesis; Ligase;

"HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97197969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification and expression of the Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP + L-tryptophan diphosphate + L-tryptophanyl-tRNA(Trp) SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
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11:1069-1075(1995).
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432 AA;
    Conservative
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Authorization (EC
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Score 1163; DB 1;
Pred. No. 1.2e-88;
1; Mismatches 100
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                                                                                                                                                          CRC64;
                                                                        Length 432;
    Indels
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                                                                                                                                                                                                                                                                           ATP-binding
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MEDLINE-21456156; PubMed-11572479;
MEDLINE-21456156; PubMed-11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Xushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
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15-JUN-2002
15-JUN-2002
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     DNA Res. 8:123-140(2001).

-i- CATALYTIC ACTIVITY: ATP + L-tryptophan + trna(Trp) = AMP + diphosphate + L-tryptophanyl-trna(Trp).

-i- SUBCELLULAR LOCATION: Cytoplasmic.

-i- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                        EMBL; AP000981; BAB65126.1; ALT INIT.
InterPro; IPR002306; Trp_tRNA-synt_1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
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thetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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Matches 189
SEQUENCE FROM N.A.

C STRAIN=ATCC 35092 / DSM 1617 / P2;

X MEDLINE=21332296; PubMed=11427726;

X MEDLINE=21332296; PubMed=11427726;

X She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A She Q., Singh R.K., Confalonieri F., Clausen I.G., Curtis B.A.,

A De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A De Moors A., Erauso G., Fletcher C., Kozera C.J., Medina N., Pen

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Pen

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup

A Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataric

I Proc. Natl Acad. Sci. U.S.A. 98:7835-7840(2001).

C -[- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +

C diphosphate + L-tryptophanyl-tRNA(Trp)

C -[- SUBCELLULAR LOCATION: Cytoplasmic.

C -[- SUBCELLULAR LOCATION: Cytoplasmic.
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TIGRFAMs; TIGR00233; trp5; 1.
PROSITE; PS00178; AA TRNA LICASE I; FALSE NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                    Sulfolobus solfataricus
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                             Tryptophanyl-tRNA
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(Rel. 41, Last annotation update)
1-tRNA synthetase (EC 6.1.1.2) (Tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357
                                                                                                                                                                                                                                                                                       Thermoprotei; Sulfolobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 910.5; DB 1
Pred. No. 7.9e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "KMSKS" REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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      SYNTHETASE
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                                                                             solfataricus
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                                                                                                                        Tolstrup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
       FAMILY
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RESULT 9
SYW PYRAB
ID SYW
AC Q9UY
DT 15-0
DT 15-0
DT 15-0
TTY
DE TTY
DE TRY
CO PYX
OC PYX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                               PYRAB
                                                                                                                                                       Q9UY11;
15-JUN-2002
15-JUN-2002
15-JUN-2002
                SEQUENCE FROM N.A. STRAIN=GE5 / Orsay;
                                                                                                                                                                                                             SYW_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006677; AAK40778.1; ALT_INIT.
InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR002305; tRNA-synt_lb.
Pfam; PF00579; tRNA-synt_lb; 1.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatic the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                   Pyrococcus abyssi.
Archaea; Euryarchaeota;
                                                                                                                 TRPS OR PABILL
                                                                                                                                          Tryptophanyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGR00233; trpS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aminoacyl-tRNA synthetase; Protein biosynthesis;
                                                       NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                   343
                                                                                                                                                                                                                                                                                                             391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEDFVDPWTVQTSSAKG-IDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFS
                                                                                                                                                                                                                                                                                                LQPLIAEHQARRKEVTDEIVKEFMTPRKLS
| : | | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                            GGQPTIELHRKYGGNPEIDVPFQWLYYFPEEDDNRIKEIEEEYRSGKWLTGELKQILIDK
                                                                                                                                                                                                                                                                                                                                                       GGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDD-KLEQIRKDYTSGAMLTGELKKALIEV
                                                                                                                                                                                                                                                                                                                                                                                             LQRDIAESLGYYKAAQIHSKFLPPLTGPEGKMSSSNPETAIYLVDDPKTVERKIMKYAFS
                                                                                                                                                                                                                                                                                                                                                                                                                     MTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRDLDLVLNDYEKSKGFFLYTGRAPSL-GMHIGHLIPFIFTKWLQEKFNANLYIBITDDB
                                                                                                                                                                                                                                                                                   LNNFLEEHR-RRREEAKELVHVFKYDGKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TESEVRATEGLDASSNIGLIFYPALQIAPT-----MFEKK---RCLIPAGIDQDPYWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TENQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFTVTPWEV----KGKVDYDKLIVQFGTQKITEELKQRIKNLAGDL-HVMLRRNVFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 AA;
                                                                                                                                       (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
1-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                             STANDARD;
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44691 MW;
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                                                                                   Thermococci;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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Pred. No. 2.2e-67;
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; CF8344CF63883680 CRC64;
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                                                                                                                                                                                                              PRT;
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                                                                                    Thermococcales;
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                                                                                                                                                                                                                                                                                   371
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                                                                                    Thermococcaceae
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                                                                                                                                       ligase)
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RESULT 10
SYW PYRHO
ID SYM P
AC 05958
DT 15-JU
DT 15-JU
DT 15-JU
DT 15-JU
DT 15-JU
DT 15-JU
DT 15-JU
DT 17Pbt
DE (Trpbt
GN TRPS
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Best Local S
Matches 173
                                                                          SYW PYRHO
059584;
15-JUN-2002
15-JUN-2002
15-JUN-2002
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submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMCILLULAR LOCATION: Cytoplasmic.
(TrpRS).
TRPS OR PH1921.
                                                   Tryptophanyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002306; Trp_trna-synt_lb.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001212; tRNA-synt_I.
Pfam; PF00579; tRNA-synt_lb; 1.
PRINTS; PR01039; TRNASYNTHTRP.
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KIQEFLKEHQKRRKKAEKQIEK 363
                                                                                                                                                                                                                                                                                                                                                                                  VLQPLIAEHQARRKEVTDEIVK 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEK 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDFKVTPWEVEGV----VDYNKLIEHFGTSPLTEELLEKTAELTKSELPLFFRRKFFFSH
                                                                                (Rel. 41,
(Rel. 41,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 AA;
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                                                                                                                                                                                             STANDARD;
                                                41, Last sequence update)41, Last annotation update)synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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45100 MW;
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"KMSKS" REGION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP000007; BAA31046.1; ALT_INIT.
InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR002305; tRNA-synt_lb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See l or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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PRINTS; PR01039; TRNASYNTHTRP.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).

SUBCELLULAR LOCATION: Cytoplasmic.

SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                    VLOPLIAEHOARRKEVTDEIVKEFMTPRKLS
                                                                                                                                                                                                                                                                TRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSG
                                                                                                                                                                                                                                                                                                                                                                   FNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRM
KIQEFLKEHQRRRKK-AEKLVEKFKYTGKLA
                                                                                                              GRPTLKEQREKGGEPEKCVVFKWLEIFFEEDDK--KLKERYYACKNGELTCGECKRYLIS
                                                                                                                                                                   GRDTIEEHROFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE
                                                                                                                                                                                                                             QRDFAESLGYYKTAALHSKFVPSLTSLSGKMSASKPETAIYLTDSPEDVEKKVWKFTLTG
                                                                                                                                                                                                                                                                                                                                         FSMAKAVFGFTEQSKIGMIFFPAIQIAPTF----FERK---RCLIPAAIDQDPYWRL
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257
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44.0%; Pred. No. 2.4e-58;
tive 68; Mismatches 125;
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8; Mismatches
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15-JUN-2002
15-JUN-2002
15-JUN-2002
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SITE
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.

Aminoacyl-tRNA synthetase; Protein biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
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STRAIN=IM2 / ATCC 51768
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Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11792869;
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LARDIADALGYPKPSTLYSKFIMALTG-ESKMSASNPDSAIYTLDDEKTVRRKV-MNAFT
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375 AA;
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
1-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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Pred. No. 2.5e-53;
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"KMSKS" REGION
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Matches 141
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A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

A Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

A Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

A Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

A Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

A Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Jung K.-H.,

A Lisenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

A Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,

"Genome sequence of Halobacterium species NRC-1.",

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

C.-I- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp).

-I- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp).

-I- SUMCELLULAR LOCATION: Cytoplasmic.

-I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                            SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE005109; AAG20355.1; -.
InterPro; IPR002306; Trp_trNA-synt_1b.
InterPro; IPR002305; trNA-synt_1.
InterPro; IPR001412; trNA-synt_1.
Pfam; PF00579; trNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
(TrpRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMs; TIGR00233; trpS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis;
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HRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDE 152
                                                          ADGNDVTPYAVESDD----LDYEKLLARFGADELTDDQRARFP-----DHPLVNRGLFYA
                                                                                                                  AEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGORPHHFLRRGIFFS
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380 AA;
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Pred. No. 9.6e-37;
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"KMSKS" REGION.
; 0F7B2B955386404F CRC64;
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(See http://www.isb-sib.ch/announce/
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Q58810;
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                   MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayron R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Xlenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                       InterPro; IPR002306; Trp_tRNA-synt_1b.
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                               EMBL; U67582; AAB99425.1; -. TIGR; MJ1415; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                           modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
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    Last sequence update)
    Last annotation update)
    synthetase (EC 6.1.1.2) (Tryptophan--trNA ligase)

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RESULT 14
SYM METTH 10 - SYM NETTH 10 - SYM NETTH 10 - 233:
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DT 15-JII
DT 15-JII
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                       STRAIN-Delta H;

MEDLINE-98037514; PubMed-9371463;

MEDLINE-98037514; PubMed-9371463;

A Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., A Harrison N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., Carusone sequence of Methanobacterium thermoautotrophicum CT "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155 (1997).

J. Bacteriol. 179:7135-7155 (1997).

C. -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + CINCELLULAR LOCATION: Cyroplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 119;
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15-JUL-1998
16-OCT-2001
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PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.

Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
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Archaea; Euryarchaeota; Methanobacteria;
Methanobacteriaceae; Methanothermobacter
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                                                                     Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon
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PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG.

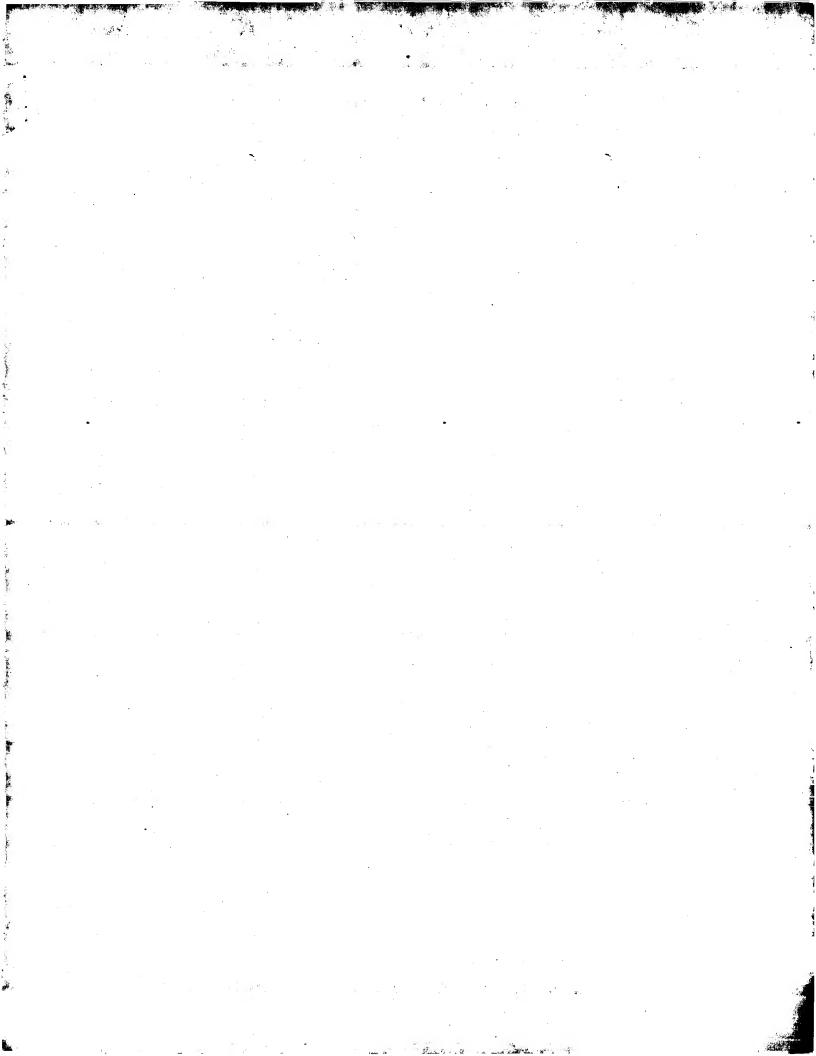
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase;
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or send an email to license@isb-sib.ch)
SEQUENCE FROM N.A.
MEDLINE=98277683; PubMed=9615449;
Peyretaillade E., Broussolle V.,
Vivares C.P.;
                                                                                                          Tryptophanyl-tRNA synthetase (TrpRS) (Fragment)
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30-MAY-2000
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PRINTS; PR01039; TRNASYNTHTRP.
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InterPro; IPR002305; TRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00579; tRNA-synt_1b; 1.
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                                                                                                                                                                                                                                                                                                                  AKI-RNAKTGGRETLKEQRELGGVPEECIIYETLLYHMSGSDSRLEEIYESCRNGTLMCG
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364 AA;
                                                                                               Conservative
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27.9%;
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Pred. No. 1.9
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"KMSKS" REGION.
; C2F348903338F61D
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               Peyret
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               Metenier G.,
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Query Match 17.2%; Score 386; DB 1; Length 134; Best Local Similarity 51.5%; Pred. No. 4.4e-25; Matches 68; Conservative 25; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ012470; CAA10034.1; ...
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00579; tRNA-synt_lb; 1.
PROSITE; P500178; AA TRNA LIGASE ; 1.
PROSITE; P500178; AA TRNA FOCEIN biosynthesis; Ligase; ATP-binding.
AMINDACY1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SITE 99 98 "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Microsporidia, amitochondrial protists, possess a 70-kDa heat shock protein gene of mitochondrial evolutionary origin.";
Mol. Biol. Evol. 15:683-689(1998).
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
       123
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                                                                                                                                                                                                                  91
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DEKFLWKSMRLE 134
                                            DEKYLWKDLTLD 162
                                                                                                                                            FAHRDFNLLLDEIANNRPFYLYTGRGPSSKTMHIGHTIPFLLCKYMQDAFKIRLVIQITD 122
                                                                                                                                                                             FSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTD 150
                                                                                                                                                                                                                                                                                    EQRITPWDVEVVSTDEVPVAIDYDKIINOFGCEKFNQALADRLEKLSGKPAHYFFRRGIV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AA; 15744 MW; 60E2935B7E1E344F CRC64;
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Search completed: July 10, 2003, 12:30:34 Job time : 10.2509 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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1 MSYKAAAGEDYKADCPPGNP......VTDEIVKEFMTPRKLSFDFQ 424
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	B	ID	Description
	2051	91.3	475	11	Q9DC65	
Ŋ	2047	91.1	481	11	Q99J58	
ω	1629	72.5	329	11	Q9D8R9	
4	1537	68.4	305	11	070184	
ហ	1382	61.5	430	σ	Q9U4Y1	
6	1379.5	61.4	420	σ	Q9U4Y0	-
7	1378	61.4	430	v	Q9VHG2	
ထ	1301	57.9	402	10	Q9SR15	
9	1027	45.7	324	ហ	Q9U1R2	
10	942	41.9	385	Ġ	Q8SQY5	
11	826.5	36.8	385	17	Q8U453	
12	800.5	35.6	490	ຫ	Q9U1F5	
13	682	30.4	136	თ	Q95295	
14	453	20.2	374	17	Q8TYF7	
15	388.5	17.3	136	σ	Q9TS88	
16	329.5	14.7	437	13	Comman	

45	44	43	42	41			38	37	36	35	34				30	29	28	27	26	25	24	23	22	21		19	18	17
130.5	134.5	135	139	140	142.5	142.5	145	145	146	148	149.5	149.5	152.5	153.5	154.5	156	158.5	164.5	167	171.5	172	181.5	188	191	274.5	286	294	310
5.8	6.0	6.0	6.2	6.2	6.3	6.3	6.5	6.5	6.5	6.6	6.7	6.7	6.8	6.8	6.9	6.9	7.1	7.3	7.4	7.6	7.7	8.1		8.5	12.2	12.7	13.1	13.8
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Q92bbl listeria in	Q9vv60 drosophila	_	Q96yv3 sulfolobus	_		Q8u2h3 pyrococcus		Q9hkt3 thermoplasm	058739 pyrococcus	Q8zw77 pyrobaculum	P93363 nicotiana t	Q9hn62 halobacteri	Q9n9b8 leishmania	Q8tsil methanosarc				Q9sgn2 arabidopsis	Q9rvd6 deinococcus					Q8txz2 methanopyru	Q9hn83 halobacteri	Q9udi5 homo sapien	Q9u533 trypanosoma	Q95yl8 encephalito

ALIGNMENTS

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"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). EMBL; AK004541; BAB23357.1;	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havashizaki Y.	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF.,	Gustincich S., Hill D., Hormann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	amanaka	Konno H., Adachi J., Fukuda	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	MEDLINE=21085660; PubMed=11217851;	STRAIN=C57BL/6J; TISSUE=LUNG:	SEQUENCE FROM N.A.	[1]	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBT TavTn-10000.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus (Mouse).		clone:1200002C07, full insert sequence.	c (II SMBLIEI. 21, Last amotation upda	(TrEMBLrel. 17,	2001 (TrEMBLrel. 17,		Q9DC65 PRELIMINARY; PRT; 475 AA.	III 1

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Best Local Similarity
Matches 383; Conserv
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Q99J58;
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01-JUN-2001
01-JUN-2002
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InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_1b.
InterPro; IPR002306; Trp_tRNA-synt_1b.
Pfam; PF00579; tRNA-synt_1b; 1.
Pfam; PF00458; MHEP-TRS; 1.
PfINTS; PR01039; TRNASYNTHTRP.
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InterPro;
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Mammalia; Eutheria;
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PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
PROSITE; PS00762; WHEP_TRS; 1.
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                           IPR002305;
IPR001412;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                   (Mouse).
etazoa; Chordata;
theria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    synthetase.
tRNA-synt_1b.
tRNA-synt_I.
Trp_tRNA-synt_1b.
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                                                                                                                                                                         WAP-TAG
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                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                         MODEL.
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Best Local S
Matches 382
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Q9D8R9;
01-JUN-2001
01-JUN-2001
01-MAR-2002
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PROSITE; P
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasererland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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Pfam; PF00458; WHEP-TRS; 1.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=PANCREAS;
MEDLINE=21085660; PubMed=11217851;
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SEQUENCE 481
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PROSITE; PS00178; AA TRNA LIGASE I;
PROSITE; PS00762; WHEP_TRS; 1.
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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AA; 54325 MW;
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Rodentia;
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90.1%; Pr
1tive 22;
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Pred. No. 1.1e-165;
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Tryptophan-tRNA synthetase (Fra-
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata; C
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But C., Fletcher C., Fujta K., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasoaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Mang K.H., Weltz C., Whittaker C., Wilming L.
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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EMBL; AK007754; BAB25235.1; -. MGD; MGI:104630; Wars.
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InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002306; Try tRNA-synt_1b.
Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNA-SYNTHTD;
PROSITE; PS00178; AA TRNA LIGASE I; 1.
SEQUENCE 329 AA; 37613 MW; 701E702DC244C4A2 CRC64;
                                                                                                                              STRAIN=HARTLEY: TISSUE=SPLEEN, Yang D., Goto R., Watanabe N., "Identification and Cloning of during DNCB-induced Guinea Pig
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                                                    Submitted (MAR-1998) to the EMBL/GenBank/DDBJEMBL; AB012222; BAA25288.1; -
                                                                                                         Reaction.";
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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"WRS-85D: A tryptophanyl-tRNA synthetase
the developing Drosophila salivary gland.
Mol. Biol. Cell 10:1595-1608(1999).
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Celniker S.;
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PETRIFO; DETAILS SYNT_1B; 1.
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WRS-95D: A tryptophanyl-tRNA synthetase expressed the developing Drosophila salivary gland.";

Mol. Biol. Cell 10:1595-1608(1999).
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Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE 430 AA; 47985
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PROSITE; PS00178; AA TRNA_LIGASE_I;
                        TIGRFAMS; TIGR00233; trpS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99250164; PubMed=10233165;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
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                                                                           PRINTS; PR01039; TRNASYNTHTRP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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  synthetase
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Pred. No. 3.
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3.6e-109;
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a; Brachycera; Muscomorpha;
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RA Adams M.D., Celniker S.E., Lolt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gebry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
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NCBI_TaxID=7227;
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MEDLINE=20196006; PubMed=10731132;
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AATS-TRP OR CG9735.
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DR FIGRPAMS; TIGR0033; TRNASYNTHTRP.
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Best Local Similarity
Matches 262; Conserv
Q9SR15;
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.

SEQUENCE 430 AA; 47971 MW; 2938EEECC69E979F
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 (TrEMBLrel. (TrEMBLrel.
                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lin X., Kaul S., Town C.D., Benito M., Creasy T.H. Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Bowman C.L., White O., Nierman W.C., Fraser C.M., "Arabidopsis thaliana chromosome III BAC F7018 ger Submitted (JAN-2001) to the EMBL/GenBank/DDBJ data
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Putative tryprophanyl-tRNA synthetase.
F7018.7 OR AT3604600.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Arabidopsis Full Length cD
Submitted (FEB-2002) to the
EMBL; AC011437; AAF04890.1;
EMBL; AY080709; AAL85027.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aminoacyl-tRNA synthetase.
SEQUENCE 402 AA; 45754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_Transport
Feam; PF00579; tRNA-synt_1b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theologis A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                       QMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVK
                                                                                                                                                                                                                                                                                                                                                                DEREAESSEQVVNPWEVSAKDGGKIDYDKLIDKFGCQRLDESLIDRVQRLTSRQPHVFLR
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                                             LTEVLTEIVERHRRARAAVTDEMVDAFMAVRPLPSMFE
                                                                                                                           KHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDXLEQIRKDYTSGAMLTGELKKA
                                                                                                                                                                                                                                      VGKCVTLNKAMGI FGFSGEDPIAKLSFPPVQAVPSFPSSFPHLFPGKDNLRCLIPCAIDQ
                                                                           LIEVLOPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ
                                                                                                           RYAFSGGQDSIEKHRELGANLEVDIPVKYLSFFLEDDSELEHIKKEYGEGRMLTGEVKKR
                                                                                                                                                                                                                                                                                                      QLTDDEKSIWKNLSVEESQRLARENAKDIIACGFDVTKTFIFSDFDYVG--GAFYKNMVK
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the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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2.5e-102;
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                                              402
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Best Local S
Matches 194
                                                                                                                                                                                                                                                                                                                                                                        Q8SQY5
Q8SQY5;
01-JUN-2002
01-JUN-2002
01-JUN-2002
Genoscope;
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[2]
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Q9U1R2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                     Tryptophanyl tRNA synthetase. ECU11_0530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                              Encephalitozoon cuniculi.
Eukaryota; Microsporidia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR002306; Trp_tRNA-synt_1b, 1.
Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
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EMBL; AL132853; CAB60439.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Harris B.R.;
                                                                                                      STRAIN=GB-M1;
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                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                  _TaxID=6035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPFFRMTRDVAPRLKASKPSLIFSTFLPALTGAQTKMSASEPNTCIFLSDTAKQIKNKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IWKVVNTNQARAIFGFTPEDCLGKAAFPAVEAAPCFASSFPQIFGKRNDIPCLIPCAIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVI
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64.9%; Pred. No. 3.
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9; Mismatches
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Q8U453;
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01-JUN-2002
01-JUN-2002
                                                                                         STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robbb F.T., Brown J.R.; Wrice Requence of the Pyrococcus furiosus genome Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE010149; AAL80365.1; - LEMBL; AE010149; AAL80365.1; - SEQUENCE 385 AA; 45178 MW; 3A7A628958200CCC CRC64;
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Nature 414:450-453 (2001).
EMBL; AL590450; CAD25963.1;
SEQUENCE 385 AA; 44188 MW; 2865C3AC95FCC859 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus
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PF0241.
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                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76;
  69;
Score 826.5; DB 1
Pred. No. 5.6e-62;
9; Mismatches 116
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Pred. No. 8
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                                             DB 17;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Tryptophanyl-trNA synthetase.
11063.04.
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01-MAY-2000
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STRAIN-FRIEDLIN;
MEDLINE-98146435; PubMed-9477341;
IVens A.C., Lewis S.M., Bagherzadd
Smith D.F.;
                                                                                                                                                                                     InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1
InterPro; IPR001316; trNA-synt_1b.
InterPro; IPR002306; Try tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
PROSITE; PR00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase.
SEQUENCE 490 AA; 54904 MW; 172C68622C511D3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania major, Eukaryota; Euglenozoa; Eukaryota; Euglenozoa; NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                    "A physical map of the Leishmania major Genome Res. 8:135-145(1998).
EMBL; AL121862; CAB58393.1; -.
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STRAIN-FRIEDLIN;
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DPSEPVQHPRDGDAGAEDVITPWVVAAKGPQGINYDRVLTIFKAERMDDGARQHMRDVMA
                                             NPAPTSNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKID-----KELIN
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                                                                                             35.6%; Score 800.5; DB 5; 37.7%; Pred. No. 1.3e-59; tive 89; Mismatches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=SMALL INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01039; TRNASYNTHTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR002306; Trp_tRNA-synt_lb.
Pfam; PF00579; tRNA-synt_lb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 281267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vinteroe A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ninteroe A.K., Fredholm M., Davies W.; Evaluation and characterization of a porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ibrary.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
  121
                                               354
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                                                                                               61
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                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                        PALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSF
                                                                                                                                                                                                                          PAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGEVKDLAADCIIREVLHDWRERRATVIDDDVVEFCRIRDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSAS-DPNSSIFLTDTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFR--DRTDIQCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIQMTDDEKYLWKDLTLDQAYGDAV--ENAKDIIACGFDINKTFIFSDLDYMGMSSGFYK
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                                               MYLTFFLEDDDKLEQI 369
                                                                                                                                                                                          PAIQXAPSESSEPQIERDRIDIQCLIPCAIDQDPYFRMTRDVXPRIGYPKPALLHSTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGELKKALIE-VLQPLIAEHQARRKEVTDEIVKEFMTPRKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIQITODEKFLFRDVPFEGAKADELIRSNIKDIIAFNFNPRHTFIFRNTHYMG---DMYP
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                                                                                                                                                                                                                                                                                                                                                                                    136
136 AA;
                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAB03585.1;
                                                                                                                                                                                                                                                                                                                                                           136
15404 MW; 951F75D1B9CD0617 CRC64;
                                                                                                                                                                                                                                                                                                        30.4%;
     136
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                    Score 682; DB 6; 1
Pred. No. 2.5e-50;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136
                                                                                                                                                                                                                                                                                                                                  DB 6; Length
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Sus.
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QBTYF
QBTYF
ID QBTYF
AC QBTYF
AC QBTYF
AC QBTYF
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 11-JU

   RESULT 15
Q9TS8
ID Q9TS8
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Best Local S
Matches 124
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Q8TYF7;
01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tryptophanyl-tRNA synthetase.
TRPS OR MK0343.
                                                                                       Q9TS88 PRELIMINARY; PRT; 136 AA.
Q9TS88;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tryptophanyl-trna-synthetase (EC 6.1.1.2) (Fragments).
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STRAIN-AV19 / DSM 6324 / JCM 9639;

MEDLINE-21927647; FubMed-11930014;

MEDLINE-21927647; FubMed-11930014;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

EMBL, AB010331, AAM01558.1;

Aminoacyl-tRNA synthetase; Complete proteome.

SEQUENCE 374 AA; 42733 MW; OBD4E5279321B828 CRC64;
                                   Eukaryota;
                                                                   Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanopyrus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 HLRLTRDIAEKEDLIKPASTYHRFMTGLTGG--KMSSSKPNTAIFLTDDPETAKEKV-WN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 YFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 WNTVKNTYGFTGETNMGHAFAPIVQAADIL---HPQ-----EIEGPHRVLVPVGVDQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 DLTLDQAYGDAVEN-AKDIIACGFDIN----KTFIFSDLDYMGMSSGFYKNVVKIQKHVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 SFLKDYNDGKLVSVLSGMMPSGR-MHLGHKTVVDQLVFYQQEMDVKVYVPIADLEAHHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 QVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KALIEVLOPLIAEHQARRKEVTDEI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKTGGGATLEEHREHGGNPDECVVYELMVYHLADRIGGDEKLREIRKKCREGDIICGECK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFSGGRDTIEEHROFGGNCDVDVSFMYLTFFLED----DDKLEQIRKDYTSGAMLTGELK 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNOVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQ-----CLIPCAIDQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMDLDRAHRIAVEEYVLNYAALGLDLDPDRCEIYLQSE-----RKTVQRMALLLAGRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDPWDVEE-----VDYERLTEEFGIRPIDEKV-----RELLPRRFPLLDRGIVFGHRDYD
      Eutheria;
                                   Metazoa;
                                                                (Bovine).
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Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.2%; Score 453; DB 17; 32.2%; Pred. No. 3.2e-30; tive 71; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Egorov Ts.A., Kazakov V.K., Musoliamov A.Kh.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos
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                                                                                                                                         244 NSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKM
                                                                                                                                                                                                                                 124 VGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDIN 183
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                                                                                                                                                                                                                                                                                             29 RATAGEDYKVDCPPGDPAPESGEGLDATEADEDFVDPWTVQTSSA------
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                                                                                               SASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDD
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Pred. No. 2.4e-25;
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1: sp_archea:*
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2116
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	5	4	u	N	1	Result No.
310	329.5	453	682	795.5	826.5	942	1027	1301	1370.5	1374.5	1374.5	1537	1629	1957	1957	Score
14.7	15.6	21.4	32.2	37.6	39.1	44.5	48.5	61.5	64.8	65.0	65.0	72.6	77.0	92.5	92.5	Query Match I
111	437	374	136	490	385	385	324	402	430	430	420	305	329	481	475	Length DB
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Q95YL8	Q8TUA1	Q8TYF7	Q95295	Q9U1F5	Q8U453	Q8SQY5	Q9U1R2	Q9SR15	Q9VHG2	Q9U4Y1	Q9U4Y0	070184	Q9D8R9	Q99J58	Q9DC65	ID
Q95yl8 encephalito	Q8tual methanosarc	Q8tyf7 methanopyru	Q95295 sus scrofa	Q9u1f5 leishmania	Q8u453 pyrococcus	Q8sqy5 encephalito	Q9u1r2 caenorhabdi	Q9sr15 arabidopsis	Q9vhg2 drosophila	Q9u4y1 drosophila	Q9u4y0 drosophila	O70184 cavia porce	Q9d8r9 mus musculu	Q99j58 mus musculu	. Q9dc65 mus musculu	Description

45	44	43	42	41	40	39	38	37	36	35	ω 4	ω	32	1	30	29	28	27	26	25	24	23	22	21	20	19	18	17
130.5	134.5	135	139	140	142.5	142.5	145	145	146	148	149.5	149.5	152.5	153.5	154.5	156	158.5	164.5	167	171.5	171.5	181.5	188	191	269.5	286	294	296.5
6. 2	6.4	6.4	6.6	6.6	6.7	6.7	6.9	6.9	6.9	7.0	7.1	7.1	7.2	7.3	7.3	7.4	7.5	7.8	7.9	8.1	8.1	8.6	8.9	9.0	12.7	13.5	13.9	14.0
419	525	365	294	337	528	375	337	332	375	316	408	327	682	317	102	372	375	895	351	385	351	331	364	324	513	109	157	136
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Q92bb1 listeria in	Q9vv60 drosophila		Q96yv3 sulfolobus			Q8u2h3 pyrococcus	Q8z0y0 salmonella	Q9hkt3 thermoplasm	058739 pyrococcus	Q8zw77 pyrobaculum	P93363 nicotiana t	Q9hn62 halobacteri	Q9n9b8 leishmania	Q8tsil methanosarc	007119 halobacteri	Q8zyt7 pyrobaculum		. Q9sgn2 arabidopsis				Q979z1 thermoplasm			Q9hn83 halobacteri		Q9u533 trypanosoma	Q9ts88 bos taurus

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InterPro; IPRO01412; trNA-synt_1.
InterPro; IPRO01412; trNA-synt_1b.
InterPro; IPRO01738; WHEP-TRS.
Pfam; PF00579; trNA-synt_1b; 1.
Pfam; PF00459; wHEP-TRS; 1.
PRINTS; PR01039; TRNA-SYNTHTRP.
TIGRPAMS; TIGR0233; trp5; 1.
PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
SEQUENCE 475 AA; 53641 MW; C3467FE85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99J58;
Q99J58;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WARS.
                          Pfam; PF00579; tRNA-synt_1b; 1.
Pfam; PF00458; WHEP-TRS; 1.
                                                                         InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR0021412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_1b.
InterPro; IPR000738; WHEP-TRS.
                                                                                                                                                                         MGD; MGI:104630; Wars.
                                                                                                                                                                                                                           Submitted (FEB-2001) to the
                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                            TISSUE-MAMMARY TUMOR.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Rodentia;
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RX Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA, Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA, Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R., RA, Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA, Ratawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R., RA, Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA, Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA, Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T., RA, Kadota K., Matsuda T., Suzuki R., Tomita M., Wagner L., Washio T., RA, Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA, Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA, Schriml L.M., Stabbli F., Suzuki R., Tomita M., Wagner L., Washio T., RA, Schriml L., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA, Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA, Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA, Baromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA, Horons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA, Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sabaski H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Ra, Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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PROSITE; PS00178; AA TRNA LIGASE I;

PROSITE; PS00762; WHEP TRS; 1.

Aminoacyl-trna synthetase.

SEQUENCE 481 AA; 54325 MW; A754)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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InterPro; IPR002306; Trp_tRNA-synt_1b.
Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
Aminoacv1-term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Tryptophan-tRNA synthetase (Fragment).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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070184;
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EMBL; AK007754; BAB25235.1; -.
MCD; MGI:104630; Wars.
InterPro; IPR002305; tRNA-synt_Ib.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                              STRAIN-HARTLEY; TISSUB-SPLEEN; Yang D., Goto R., Watanabe N., Kobayashi Y.; Yang D., Goto R., Watanabe N., Kobayashi Y.; "Identification and Cloning of Genes Whose Expressions are Elevated during DNCB-induc,ed Guinea Pig Skin Delayed-type Hypersensitivity
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Pfam; PF00579; tRNA-Synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
SEQUENCE 329 AA; 37613 MW; 701E702DC244C4A2 CRC64;
                                                                              SEQUENCE
                                                                                                         Aminoacyl-tRNA synthetase.
NON_TER 1 1
                                                                                                                                                                                                                                                                                   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                      Reaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                34838 MW;
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92.1%;
  72.6%;
94.4%;
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Pred. No. 2.7e-131;
7; Mismatches 9;
Score 1537; DB 11;
Pred. No. 1.8e-123;
                                                                              0937164333780EB7
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                                                                                                                                                                                             Query Match
Best Local S
Matches 254
                                                                                                                                                                                                                                                                                                                                                      Seshalah P., Andrew D.J.;

"MRS-85D: A tryptophanyl-trNA synthetase expressed to the developing Drosophila salivary gland.";

L Mol. Biol. Cell 10:1595-1608(1999).

R MBL; AFI25157; AAF20167.1; -.

FlyBase; FBgn0010803; Aats-trp.

R InterPro; IPR002305; TRNA-synt_1b.

R InterPro; IPR002305; Trp tRNA-synt_1b.

R InterPro; IPR002306; Trp tRNA-synt_1b.

R Pfam; PF00579; tRNA-synt_1b; 1.

R PRINTS; PR01039; TRNA-SYNTHTRP.

R PRINTS; PR01039; TRNA-SYNTHTRP.

R TICHPAMS; TICH00233; trpS; 1.

R PROSITE; PS00178; AA TRNA LICHSE_1; 1.
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Q9U4Y0;
01-MAY-2000
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso:

Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Tryptophanyl-tRNA synthetase (Fragment).
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                                                                                                                                                                                                                                                                                                                     Aminoacyl-tRNA synthetase.
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                                                                                            ATAPTEDVVDPWNVASSNDAGVDYDKLIKRFGSSKIDBELIARFEKITGKPAHHFIRRGM
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                                                                                                                                                                                          Score 1374.5; DB 5;
Pred. No. 2.4e-109;
51; Mismatches 76;
                                                                                                                                                                                                                                                                                              4AF7088AF426AEB6 CRC64;
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Matches 254
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Q9U4Y1;
01-MAY-2000
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EMBL; AF125156; AAF20166.1; -.
EMBL; AY075249; AAL68116.1; -.
FlyBase; FBgn0010803; Aats-trp.
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1b.
Ffam; PF00579; tRNA-synt_1b.
Ffam; PF00579; tRNA-synt_1b; 1.
FRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Par Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miranda A., Mungarr Patel S., Phouanenavong S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seshaiah P., Andrew D.J.;
"WRS-85D: A tryptophanyl-tRNA synthetase expressed the developing Drosophila salivary gland.";
Mol. Biol. Cell 10:1595-1608(1999).
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR00233; trps; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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Celniker S.;
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FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMT 126
                                ATAPTEDVVDPWNVASSNDAGVDYDKLIKRFGSSKIDEELIARFEKITGKPAHHFIRRGM
                                                                                                  ATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
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DDEKTLWKDLKVEDAIKLGRENAKDIVAIGFDVNKTFIFNNLEFVGKCPAMYQNIIRIQK
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                                                                                                                                                              Conservative
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(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                         synthetase.
                                                                                                                                                                                                                                                                47985 MW;
                                                                                                                                                                                    65.0%; Score 1374.5; 64.8%; Pred. No. 2.5e
                                                                                                                                                         61;
                                                                                                                                   Pred. No. 2.5e-109;
l; Mismatches 76;
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Choston K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shie B. C., Staller Kiamos I., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative tryptophanyl-tRNA synthetase.
F7018.7 OR AT3G04600.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicareae.
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BMBL, AB003682, AAG22136.1; -.
STRAIN=CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thalfana chromosome III BAC F7018 genomic seque
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1
InterPro; IPR002306; Trp tRNA-synt_1b.
Pfam; PF00579; tRNA-synt_1b; 1.
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TIGRFAMS; TIGR00233; trpS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
SEQUENCE 430 AA; 47971 MW; 2938EEECC69E979F CRC64;
                                                                                                                                                             SEQUENCE FROM N.A.
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InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_1b.
InterPro; IPR002306; Trp_tRNA-synt_1b.
IPR00579; tRNA-synt_1b; 1.
IPRNTS; PR01039; TRNASYNTHTRP.
TIGFPAMS; TIGR00233; trpS; 1.
IPROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Amiloacyi-tRNA synthetase.
SEQUENCE 402 AA; 45754 MW; B9BEA75EE
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Q9U1R2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
                          SEQUENCE
Harris B.
                                                                                            Eukaryota; Metazoa; Nematoda; Rhabditidae; Peloderinae; Caer MCBI_TaxID=6239;
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Submitted (FB-2002) to the EMBL/GenBan
EMBL; AC01437; AAF04890.1;
EMBL; AV080709; AAL85027.1;
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  Submitted
                                                                                                                                                                           Caenorhabditis elegans.
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SEQUENCE FROM
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  (SEP-1999)
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the
                                                                                                                            oda; Chromadorea; Caenorhabditis.
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  EMBL/GenBank/DDBJ
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Last annotation updat
                                                                                                                                                                                                                                                                                                     Created)
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RESULT 10
Q8SQY
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AC Q8SQY
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Query Match
Best Local S
Matches 179
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Best Local
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                                                                                  MEDLINE-21576510; PubMed-11719806;
Katinka M.D., Duprat S., Cornillot E., Mete Prensier G., Barbe V., Peyretailade E., Barbe Prensier G., Barbe V., Peyret P., Saurin Weissenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the Encephalitozoon cuniculi.";
Nature 414:450-453 (201).
EMBL; AL590450; CAD25963.1; -. SEQUENCE 385 AA; 44188 MW; 2865C3AC95FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8SQY5;
Q8SQY5;
01-JUN-2002
01-JUN-2002
01-JUN-2002
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EMBL, AL132883; CAB60439.1; -
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR002306; Trp_tRNA-synt_1b.
Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Encephalitozoon cuniculi.
Eukaryota; Microsporidia;
NCBL_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tryptophanyl tRNA synthetase. ECU11_0530.
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SEQUENCE FROM N.A.
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                             STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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  179;
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                      44.5%;
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  76;
Score 942; DB
Pred. No. 2.3e
76; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
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Pred. No. 9.6e-80;
9; Mismatches 64;
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                                                                                                                                                                                                                    , Metenier G., Th
E., Brottier P.,
aurin W., Gouy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385
                                                                                                                                                                             the
DB 5; 1
2.3e-72;
1es 123;
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Best Local Similarity
Matches 180; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=VCI / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; Bubmitted (FEB-2002) to the EMBL/GenBank/DDBJ data EMBL; ABO10149; AAL80365.1; -

Aminoacyl-ENDA synthetase; Complete proteome.
SEQUENCE 385 AA; 45178 MW; 3A7A628958200CCC CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8U453
Q8U453;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                             EEDF-VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTD
|:||| |:|| |:|| :|| :|| :|| :|| :|| |:||
FAHRDFNLLLDEIANNRPFYLYTGRGPSSKTWHIGHTIPFLLCKYMQDAFKIRLVIQITD
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                                                                                                                                 KYLWKD-LTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHV
                                                                                                                                                                                                   HRDYDKVLDDYEQGKGFFLYTGRGPSG-PMHIGHIIPFFATKWLQEKFDVNLYIQITDDE
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NFSMAKAVFGFTEQSKIGMIFFPAIQAAPTF---
                                          TENQVKGIFGFTDSDCIGKISEPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFR
                                                                                                                                                                                                                                                                                                       ESEFKVTPWEVEGI----IDYNKLIEQFGTSPLTDDLLERTARLTKSELPIFFRRKFFFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIFCAIDQDPYF
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                                                                                                 KFLFKENLTFEDTKYWAYQNILDIIAVGFDPDKTFIFQNSEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGRKTLEEHREKGGDIDVDVPFEYLKYFLDDDQELEKYRSGYIKGEITSKEMKEKCVVV
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 39.1%; Score 826.5; 45.9%; Pred. No. 1.8
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21,
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                                                                                                                                                                                                                                                                                                                                                                                                      69;
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W; 3A7A628958200CCC CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 116;
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  FEKK---RCLIPAAIDQDPYWR
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                                                                                                    TKIYEMAIPIAKKI
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Best Local S
Matches 173
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O9U1F5
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TREMBLEL. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       "A physical map of the Leishmania major Genome Res. 8:135-145(1998).

EMBL, ALIZ1862: CAB58393.1; -.

InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.

InterPro; IPR001306; Trp tRNA-synt_1b.

Pfam; PF00579; tRNA-synt_b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania major.
Eukaryota; Euglenozoa;
EURI TaxID=5664;
                                                                                                                                                                                                                                                                                                      Aminoacyl-tRNA synthetase.
SEQUENCE 490 AA; 54904 MW;
                                                                                                                                                                                                                                                                                                                           Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bothe G., Pohl T., Ivens A.C., Lawson D., Quail M., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tryptophanyl-tRNA synthetase. L1063.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                     Similarity
                              HVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFR--DRTDIQCLIFCAIDQD 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQRDFAESLGYYKTAALHSKFFPPLTGLEGKMSASKPETAIYLTDNPEEAGKKIWKFALT
                                                                                                                          NQVLDAYE----NKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDD
                                                                                                                                                         TTTPSANAEGVATPVLDAVPAGDAALQAAASPAMQQRQQPPALALHHFFHRDIAFSHRDL
                                                                                                                                                                        HPRDGDAGAEDVITPWVVAAKGPQGINYDRVLTIFKAERMDDGARQHMRDVMAKCRKRTM
                                                                                                                                                                                                                       HGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKID------KELINRIERAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORVOEFLKEHOEKRKK-AEKLVEKFKYTGKLA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALI
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                                                                                 EKYLWKDLTLDQAYGDAV--ENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQK 186
                                                                                                         HKALVDI EASVKTGERSVFLYTGRGPSAGTMHLGHVLPFMLTKYLQDVFSLPLVIQITDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGQPTLKEQREKGGNPEKCVVFKWLEIFFEPDDK--KLMERYYACKNGELLCGECKRYLI
            SMTGNAVKHTLGITDSDNVGKLAFPATQAAPCFSTAFRRVLRNGDR-PMRCLIPCAIDQD
                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bagherzadeh
                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                       Score 795.5; DB 5;
Pred. No. 1.2e-59;
7; Mismatches 129;
                                                                                                                                                                                                                                                                                                         172C68622C511D3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Α.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                 Friedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                       L., Chan H.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                                                                                                                                                                genome.";
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                                                            --DMYPTVLRLQR
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RESULT 14
QRIYF
ID QRIYF
AC QRIYF
AC QRIYF
DT 01-JU
DT 01-JU
DT 01-JU
DT 17PPt
GN TRPS
OS Metha
OC Archa
OC Metha
OC NCBI
RN [1]
RN [1]
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QSTYF7;

PRELIMINARY;

374

B

01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
Tryptophanyl-trNA synthetase.
TRPS OR MK0343.

Last sequence update)
Last annotation update)

NCBI_TaxID=2320;

SEQUENCE FROM N.A.

Methanopyrus kandleri. Archaea; Euryarchaeota;

Methanopyri;

Methanopyrales; Methanopyraceae;

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Q9529
AC Q9529
AC Q9529
AC Q9529
DT 01-FE
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DT 01-FE
DT 01-JU
DE TYPE
COC EUKas
OC EUKas
OC EUKas
OC Mamma
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RR TISSU
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DR EMBL;
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Best Local :
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NON_TER
SEQUENCE
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InterPro; IPR002305; tRNA-synt lb.
InterPro; IPR002306; Trp_tRNA-synt_lb.
Pfam; PP00579; tRNA-synt lb; 1.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                      TISSUE-SMALL INTESTINE; Winteroe A.K., Fredholm M., Davies W.; "Evaluation and characterization of a library.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95295;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequei
01-JUN-2002 (TrEMBLrel. 21, Last annot:
Tryptophanyl-tRNA synthase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95295
                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A
 121
                          331
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                                                                                                                                                                                 32.2%;
Similarity 94.1%;
                                                                                                                             PAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFF
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MYLTFFLEDDDRXEQI
                MYLTFFLEDDDKLEQI 346
                                                                        PALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSF
                                                                                                           PAIQXAPSFSSSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVXPRIGYPKPALLHSTFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIE-VLQPLIAEHQARRKEVTDEIVKEFMTPRKL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRAFSGGCATLEOMOETGANLELDVAYOYLRFFCPDDTLFADVTQRYRSGTLNSGEVKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALQGAQTKMSXXAPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSF
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136 AA;
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                           15404 MW;
136
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                                                                                                                                                                  Score 682; DB 6
Pred. No. 1e-50;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                           951F75D1B9CD0617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136
                                                                                                                                                                                                                                                                                                                                                                     porcine
                                                                                                                                                                                              DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                   6;
                                                                                                                                                                                                                                                                                                                                                                      small intestine
                                                                                                                                                                                            Length 136;
                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                     Indels
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Sus.
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                                                                                                                                                                   Gaps
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QSTUAT 15
QSTUAN
ID QSTUA
AC QSTUA
AC QSTUA
DT 01-JU
DT 01-JU
DT 17Ppt
GN TRPS
GN TRPS
OS Metha
OC Archa
OC Metha
OC META
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Best Local S
Matches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TUA1;
01-JUN-2002
01-JUN-2002
01-JUN-2002
Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Paulsen I., Jarrell K.F., Swanson R.V., Zinder S.H., Lander E.,
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MEDLINE=21927647; PubMed=11930014;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

EMBL, AE010331; AAM01558.1; -
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-C2A / ATCC 35395 / DSM 2834;

MEDLINE-21929760; PubMed=11932238;

MEDLINE-21929760; PubMed=1032238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanosarcina acetivorans.
Archaea; Euryarchaeota; Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tryptophanyl-tRNA synthetase. TRPS OR MA0172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAUL85
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SEQUENCE 374 AA; 42733 MW; 0BD4E5279321B828
                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanosarcinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                            TaxID=2214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanosarcina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanococci;
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Aminoacyl-tRNA synthetase; Complete proteome.
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FEBS Lett. 300:162-166(1952).
-I- CATALYTIC ACTIVITY: ATP + L-tryptophan +
diphosphate + L-tryptophanyl-tRNA(Trp).
-I- SUBUNIT: HOMODIMER.
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"The human gene encoding tryptophanyl-tRNA synthetase: interf
response elements and exon-intron organization.";
Gene 128:237-245(1993).
                                                               TIGREAMS; TIGR00233; trpS; 1.
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PROSITE; PS00762; WHEP TRS; 1.
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"An interferon-induced protein with release factor activity is
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, K62570, CAAA4450.1;
, K62570, CAB94198.1;
, K67920, CAB94198.1;
, K67921, CAB94198.1;
, K67922, CAB94199.1;
, K67923, CAB94199.1;
, K67924, CAB94199.1;
, K67925, CAB94199.1;
, K67926, CAB94199.1;
, K67927, CAB94199.1;
, K67928, CAB94199.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO CLASS-I F
SIMILARITY: CONTAINS 1 WHEP-TRS
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                                                                                                                                                                                                                      HGNC:12729; WARS.
                                                                                                                                                   IPR002306; Trp_tRNA-synt_lb.
IPR000738; WHEP-TRS.
IPR002305; tRNA-synt_lb.
IPR001412; tRNA-synt_I.
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"KMSKS" REGION.

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Best Local
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01-AUG-1990
01-MAY-1992
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
(TrpRS).
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                                                                                   Labouesse J., Bonnet J.;
Submitted (MAR-1990) to the EMBL/GenBank/DDBJ
-i- CATALYTIC ACTIVITY: ATP + L-tryptophan + t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                       Garret M., Trezeguet V., Pajor
Guegueiv M., Benedetto J.-P.,
                                                                                                                                                                                                                                                                               Biochemistry 30:7809-7817(1991).
                                                                                                                                                                                                                                                                                                      chain release
                                                                                                                                                                                                                                                                                                                     "A mammalian tryptophanyl-tRNA synthetase shows little homology prokaryotic synthetases but near identity with mammalian peptide
                                                                                                                                                                                                                                                                                                                                                                     Gandar J.-C., Benedetto J.-P., Sallafranque Gueguen M., Sarger C., Labouesse B., Bonnet
                                                                                                                                                                                                                                                                                                                                                                                             Garret M., Pajot B., Gandar J.-C., Benedet
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91329348; PubMed=1907847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
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                                                                                                                                                                                                           TISSUE=Pancreas;
                                                                                                                                                                                                                                 SEQUENCE OF 17-475
    diphosphate + L-tryptophanyl-tRNA(Trp).
SUBUNIT: HOMODINER.
SIMILARITY: BELONGS TO CLASS-I AMINAACY
SIMILARITY: OCC.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
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er C., Alteriot
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                                                                                                                                                         Merle
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RESULT 3
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Best Local (
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EMBL; X52113; CAA36356.1; -.
PIR; A40279; YWBO'
PIR; S14540; S14540.
InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001312; tRNA-synt_l.
SYM RABIT STANDARD,
SYM RABIT STANDARD,
SYM RABIT STANDARD,
SYM RABIT STANDARD,
P23612; Q28607;
01-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00458; WHEP-TRS; 1.
Pfam; PF00579; tRNA-synt_1b; 1
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.

PROSITE; PS00762; WHEP_TRS; 1.

Aminoacyl-trNA synthetase; Protein_biosynthesis; Ligase; ATP-binding.
                                                                                                                                                                                                                                                                   435
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                                                                                                                                                                                                                                                                                                                                                                     KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIFCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
                                                                                                                                                                                                                                                                 KKELIEVLOPLIAEHOARRKEVTDEIVKEFMTPRKLSYDFO
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                                                                                                                                                                                                                                                                                                                                                  KVNKHAFSGGRDTVEEHROFGGNCDVDVSFMYLTFFLEDDDKLEQIRRDYTSGAMLTGEL
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117
178
357
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L -> M (IN REF. 2).
; F7E531750137EB32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2028.5; DB 1
Pred. No. 2.6e-159;
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SITE
SITE
                                                                                                                                                                                                                                                                                                                        TIGRFAMS;
PROSITE; P
PROSITE; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mammalian polypeptide chain release factor and tryptophanyl-trna synthetase are distinct proteins.";
EMBO J. 12.4013.4019(1993).

-i- CATALYTIC ACTIVITY: ATP + L-tryptophan + trna(Trp) = AMP + diphosphate + L-tryptophanyl-trna(Trp).

-i- SUBUNIT: HOMODIMER (BY SIMILARITY).

-i- SUBUNIT: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

-i- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
REVISIONS TO 169-174 AND 227-228, AND FUNCTION MEDLINE=94009008; PubMed=8404867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90239043; PubMed=2185472;
Lee C.C., Craigen W.J., Muzny D.M., Harlow E., Caskey C.T.;
"Cloning and expression of a mammalian peptide chain release
with sequence similarity to tryptophanyl-tRNA synthetases.";
Proc. Natl. Acad. Sci. U.S.A. 87:3508-3512(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00458; WHEP-TRS; 1. Pfam; PF00579; tRNA-synt_lb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M33460; AAA31246.1; ALT_SEQ.
EMBL; U02595; AAB60257.1; -.
PIR; A35904; YWRBPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frolova L.Y., Dalphin M.E., Justesen J., Powell R.J., McCaughan K.K., Kisselev L.L., Tate W.P., Haenni A.-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR00233; trpS; 1.

PROSITE; PS00178; AA TRNA LIGASE_I; 1.

PROSITE; PS00762; WHEP_TRS; 1.

Aminoacyl-trna synthetase; Protein_biosynthesis; Ligase; ATP-binding.
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                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR000738; WHEP-TRS.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAUTION: WAS ORIGINALLY (REF.1) THOUGHT RELEASE FACTOR (ERF).
                181
                                           195
                                                                    121
                                                                                               135
                                                                                                                        61
                                                                                                                                                                                                      367;
                                                                                                                                                  75
                                                                                                                                                                          N
                                                                                                                                                                                                                  Similarity
VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                         LVIQMTDDEKYLMKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                  FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                                  SHGDPEAVDDKEDFVDPWTVRTSSAKGIDYDKLIVQFGSSKIDKELVNRIERATGQRPHR
                                                                                                                                                               NHG-PDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 60
                                         LVVQMSDDEKYLWKDLTLEQVYGYTLENAKDIIACGFDVNKTFIFSDLDYMGMSPGFYKN
                                                                                             FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFDVP
                                                                                                                                                                                                                                                        168
353
475 AA;
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177 "I
357 "I
53799 MW;
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20; Mismatches
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"KMSKS" REGION
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                                                                                                                                                                                                     .5e-154;
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                                                                                                                                                                                                                                                                                              by non-profit institute. There are no restrictions on modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.and.for.commercentities and memail to license
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P32921;
                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                           -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: The short isoform is widely expressed, the long form is found only in embryonic stem cells.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-!- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pajot B., Sarger C., Bonnet J., Garret M.;
"An alternative splicing modifies the C-terminal end
"RNA synthetase in murine embryonic stem cells.";
Alternative splicing.
DOMAIN 23 68
SITE 168 177
                                                         TIGREAMS; TIGR00233; trpS; 1.

PROSITE; PS00178; AA TRNA LIGASE_I; 1.

PROSITE; PS00762; WHEP_TRS; 1.
                                                                                                     Pfam; PF00458; WHEP-TRS; 1.
Pfam; PF00579; tRNA-synt lb; 1.
PRINTS; PR01039; TRNASYNTHTRP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993
15-JUN-2002
                                                                                                                                             InterPro; IPR002396; Trp tRNA-synt ib.
InterPro; IPR000738; WHEP-TRS.
InterPro; IPR002305; tRNA-synt lb.
InterPro; IPR001412; tRNA-synt I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95018226; PubMed=7932716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WARS OR WRS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993
                                            Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                             MGI:104630; Wars.
                                                                                                                                                                                                                             $31461; $31461.
$31462; $31462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 27, Last sequence update)
(Rel./41, Last annotation update)
l-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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                                            Protein biosynthesis; Ligase; ATP-binding
"HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RX MEDLINE=21848401; PubMed=11859360;
RA MEDLINE=21848401; PubMed=11859360;
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.N.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Wa Meltjens I., Vanstreels E., Rieger M., Schaefer M., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Wa Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
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VARSPLIC
SEQUENCE
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Q09692;
Q1-NOV-1995 (Rel. 32, Created)
Q1-NOV-1995 (Rel. 32, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Putative tryptophanyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligase) (TrpRS).
SPAC2F7.13C.
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476
481 AA;
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scomycota; Schizosaccharomycetes;
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Pred. No. 7.4e-152;
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(EC 6.1.1.2) (Tryptophan--tRNA
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RESULT 6
SYWC_YEAST
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Best Local
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-i- CAPALYTIC ACTIVITY: ATP + L-tryptophan + tRNA (Trp) = AMP + diphosphate + L-tryptophanyl-tRNA (Trp).
SYWC YEAST STANDARD;
Q12109;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SITE 91 1
SITE 275 2
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TIGREAMS; TIGRO0233; trpps; 1.
PROSTITE; PS00178; AA TRNA LIGASE I; 1.
Hypothetical protein; Aminoacyl-trNA synthetase;
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InterPro; IPR002305; TRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00579; tRNA-synt_1b; 1.
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                                                                                                                                                                                             EVLQPLIAEHQARRKEVTDEIVKEFMT-PRKLSF
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                                                                                                                                                                     KLLQQFVSDFQAARSKVDEATLDMFMDGSRKLEW 395
                                                                                                                                                                                                                                                                                                      AFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALI
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"KMSKS" REGION.
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Pred. No. 4.2e-92
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TIGREPAMS; TIGRO0233; trpS; 1.
PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SITE "HIGH" REGION.
SITE "WASKS" REGION.
SITE "WASKS" REGION.
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"Identification and expression of the Saccharomyces cytoplasmic tryptophanyl-tRNA synthetase gene.";
Yeast 13:37-41(1997).
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EMBL; Z74839; CAA99110.1; -.
SGD; S0005457; WRS1.
InterPro; IPR002306; Trp_tRNA-synt_1b.
InterPro; IPR002305; TRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1.
Pfam; PF00579; tRNA-synt_1b; 1.
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Yeast 11:1069-1075(1995).
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MEDLINE=96076631; PubMed=7502582;

Vandenbol M., Durand P., Portetelle D., Hilger F.;

Vandenbol M., Durand P., Portetelle D., Hilger F.;

"Sequence analysis of a 44 kb DNA fragment of yeast chromosome including the Tyl-H3 retrotransposon, the suf1(+) frameshift suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-la and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccisaccharomycetales; Saccharomycetaceae; Saccharomyces
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01-NOV-1997 (Rel. 35, Last annotation update)
Tryptophanyl-tRNA synthetase, cytoplasmic (EC
tRNA ligase) (TrDRS).
WRS1 OR YOL097C OR HRE432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                          VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                    VIELTDDEKFLFKHKLTINDVKNFARENAKDIIAVGFDFKNTFIFSDLQYMG--GAFYET
                                                                                                         VIQMTDDEKYLWK-DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                              STDVKBQVVTPWDVEGGVDEQGRAQNIDYDKLIKQFGTKPVNEETLKRFKQVTGREPHHF
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54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Mismatches 100;
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Pred. No. 3.5e-88;
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RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140 (2001).
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-rRNA(Trp).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=JCM 10545 / 7;

MEDLINE=21456156; PubMed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Kawarabayasi Y., Hino Y., Horikawa H., Hosoyama A., Fukui S.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Sekine M., Baba S.-I., Ankai A., Nakazawa H., Takamiya M., Kato Y.,

Nagai Y., Nishijina K., Otsuka R., Nakazawa H., Takamiya M., Oguchi A.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002305; tRNA-synt_ib. Pfam; PF00579; tRNA-synt_ib; 1.
Pfam; PF00579; tRNA-synt_ib; 1.
TIGRPAMs; TIGR00233; trpS; 1.
PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase;
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Archaea; Crenarchaeota;
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15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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or send an email to license@isb-sib.ch).
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QDFNVTPWEV-----KGKVDYDKLIVQFGTQKITSELKEKIKSIINDELHVMLRRDVFFS
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IPR002305; tRNA-synt_1b.
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381 /
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                                                                                                            63;
                                                                                                            Score 910.5; DB
Pred. No. 1.7e-67
3; Mismatches 9
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"KMSKS" REGION
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A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
D Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
A Charlebois R.L., Doolittle W.F., Duguet M., Gasserland T.,
Charlebois R.L., Doolittle W.F., Duguet M., Gasserland T.,
A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
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STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
                                                                                                                                                                                       EMBL; AE006677; AAK40778.1; ALT_INIT.
InterPro; IPR002306; Trp_tRNA-synt_lb
                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
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(Rel. 41, Last sequence update)

(Rel. 41, Last annotation update)

1-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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PRINTS; PR01039;

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Pfam; PF00579;

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                                                                                                                                                                                                "Pyrococcus abyssi genome sequence: insights into archaeal ch structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEDFVDPWTVQTSSAKG-IDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFSEVRATFGLDASSNIGLIFYPALQIAPT-----MFEKK----RCLIPAGIDQDPYWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYMRNPEFTLDQTRSWAYDNILDIIAVGFNPDKTFIFQDTEYI---RNMYPITVKIAKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOPLIAEHOARRKEVTDEIVKEFMTPRKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LORDIAESLGYYKAAOIHSKFLPPLTGPEGKMSSSNPETAIYLVDDPKTVERKIMKYAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41, Created)
41, Last sequence update)
41, Last sequence update)
41, Last annotation update)
synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.8%;
48.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 905; DB 1;
Pred. No. 4.8e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "HIGH" REGION.
"KMSKS" REGION.
; CF8344CF63883680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385
                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108;
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                                                                                         restrictions on
tent is in no
                                                                                                                               EMBL outstation
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                                                                                                                                                      a collaboration
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RESULT 10
SYW_PYRHO
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Best Local S
Matches 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete
SITE
SITE
SEQUENCE
MEDLINE-98344137; PubMed-9679194; Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Kawarabayasi Y., Sawada M., Horikawa H., Hosoyama A., Nagai Y. Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y. Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H., Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                     SYW_PYRHO
059584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002306; Trp_tRNA-synt_1b.
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1.
Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                          SEQUENCE FROM N.A. STRAIN=OT3;
                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tr
                                                                                                                                                                                           Pyrococcus horikoshii.
Archaea; Euryarchaeota;
                                                                                                                                                                                                         TRPS OR PH1921.
Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMs; TIGRO0233; trpS; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ248288; CAB50601.1;
                                                                                                                                                                  NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                              367
                                                                                                                                                                                                                                                                                                                                                                                                                                           284
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GRPTLKEQREKGGEPEKCVVFKWLEIFFEEDDK--KLKERYYACKNGELTCGECKRYLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRDFAESLGYYKTAAIHSKFVPSLTSLSGKMSASKPETAIYLTDSPEDVEKKVWKFALTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLFKENLTFEDTKHWAYENILDIIAVGFDPDKTFIFQNSEF----TKIYEMAIPIAKKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDF-VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome.
                                                                                                                                                                                                                                                                                                                                                                                                            VLQPLIAEHQARRKEVTDEIVK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDYDKVLQDYEEGRGFFLYTGRGPSG-PMHIGHIIPFFATKWLQEKFGVNLYIQITDDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDFKVTPWEVEGV----VDYNKLIEHFGTSPLTEELLEKTABLTKSBLPLFFRRKFFFSH
                                                                                                                                                                                                                                                                                                                                                                                     KIQEFLKEHQKRRKKAEKQIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSMAKAVFGFTEQSKIGMIFFPAIQIAPTF-----FEKR---RCLIPAAIDQDPYWRL
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253
385 AA;
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                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 "1
257 "1
45100 MW;
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                                                                                                                                                                                           Thermococci;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 803; DB 1;
Pred. No. 1.2e-58;
3; Mismatches 120
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"KMSKS" REGION.
; 4C29D01414976B12
                                                                                                                                                                                            Thermococcales;
                                                                                                                                                                                                                                                                                                                   386
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                                                                                                                                                                                                                                               (Tryptophan--tRNA ligase)
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                                                                                                                                                                                           Thermococcaceae;
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SYM_PYRAE
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ID SYM II
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Best Local S
Matches 172
                                                                                                                                                                                                        082TU5;
15-JUN-2002
15-JUN-2002
15-JUN-2002
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Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
SITE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00579; tRNA-symt 1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
PROSITE; P800178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; ProteIn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                            Tryptophanyl-tRNA
                                                                                                                                                                                                                                                                                                                           SYW_PYRAE
                                                                                                                      TRPS OR PAE3091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
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CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).

SUBCELLULAR LOCATION: Cytoplasmic.

SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 KIQEFLKEHORRRKK-AEKLVEKFKYTGKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 TRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSJFLTDTAKQIKTKVNKHAFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 YLWKD-LTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
172; Conserv
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Query Match
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InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001212; tRNA-synt_l.
TIGREPAMS; TIGR00233; trpS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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SUBCELLULAR LOCATION: Cytoplasmic.
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375 AA;
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  374
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WA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

WA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

WA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

WA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

WA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

WA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

WA Maddocks D.G., Jablonski P.E., Krebs M.P., Agudich J.L., Jung K.-H.,

WA Maddocks D.G., Jablonski P.E., Krebs M.P., Agudich J.L., Jung K.-H.,

WA Maddocks D.G., Jablonski P.E., Krebs M.P., Agudich J.L., Jung K.-H.,

WA Maddocks D.G., Jablonski P.E., Krebs M.P., Agudich J.L., Jung K.-H.,

WA Maddocks D.G., Jablonski P.P., Omer A.D.,

WA Maddocks D.G., Welling P.P., Omer A.D.,

WA Maddocks D.G., Welling P.P., Omer A.D.,

WA Maddocks D.G., Welling P.P., Omer A.D.,

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WA Maddocks D.G., Welling P.P., Omer A.D.,

WA Maddocks D.G., Welling P.P., Maddocks P.P.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMs; TIGR00233; trpS; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRPS OR TRPS2 OR VNG2232G.
Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001411; tRNA-synt_I.
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Tryptophanyl-tRNA synthetase
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NKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDD-KLEQIRKDYTSGAMLTGELK 361
                                                                                                                                                                                                                                                                                                                                                                           KYWFKDQTPAET-GDYLRANLRDLLAVGFDPELTRIVVDTRDADVLYPLATAFAGDV----
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                                                                                                                                               PYFRMTRDVAPRIGYP--KPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYLWKDLTLDQAYGDAVE-NAKDIIACGFDINKTFIF---SDLDYM-GMSSGFYKNVVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADGNDVTPYAVESDD----LDYEKLLARFGADELTDDQRARFP-----DHPLVNRGLFYA
                                                                           PHVRVSRDVAAKARYPVGKPGALLMQFLPSLAG-PGKMSSS-AGVSIRLTDSPDTVREKV
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35.4%;
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|thetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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"KMSKS" REGION.
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Matches 119
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01-NOV-1997 (Rel. 35, L
16-OCT-2001 (Rel. 40, La
Tryptophanyl-tRNA synthe
(TrpRS).
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01-NOV-1997
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SITE
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MEDINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYW_METJA
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00579; tRNA-synt_lb; 1.
PRINTS; PR01039; TRNASYNTHTRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U67582; AAB99425.1; -. TIGR; MJ1415; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRPS OR MJ1415.
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Aminoacyl-tRNA synthetase; Proteïn biosynthesis; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362
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                                                        17
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                                                                                                                                     Similarity
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PW--ETPAV--IDYKKTMEQFGVKPIVDVLGDLKEE---
                                                     PWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQV 76
                                                                                                                                                                                                                                                                                                proteome.
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                                                                                                                                                                                                                                                                                                                                                                                     TIGR00233; trps; 1.
                                                                                                                                                                                                                    255
370 AA;
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    Last sequence update)
    Last annotation update)
    synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)

                                                                                                                                                                                                                       42660
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                                                                                                                                     19.4%;
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                                                                                                        Score 409.5; DB 1;
Pred. No. 2.6e-26;
72; Mismatches 153;
                                                                                                                                                                                                                                             "HIGH" REGION
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A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
A Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
T'Complete genome sequence of Methanobacterium thermoautotrophicum
T deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
C --- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
C diphosphate + L-tryptophanyl-ERNA(Trp).
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    -!- SUBCELLULAR LOCATION: Cytoplasmic.
    -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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NCBI_TaxID=187420;
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Archaea; Euryarchaeota; Methanobacteria;
                                     Pfam;
                                                                                                        EMBL; AE000812; AAB84757.1;
                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                               the European Bioinformatics Institute.
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                PRINTS; PR01039;
                                                                       InterPro;
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                                                    InterPro; IPR001412; tRNA-synt
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                                                                 IPR002306; Trp_tRNA-synt_1b.
IPR002305; tRNA-synt_1b.

    (Rel. 36, Created)
    (Rel. 36, Last sequence update)
    (Rel. 40, Last annotation update)
    1-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)

                  tRNA-synt_1b;
9; TRNASYNTHTRP
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Best Local S
Matches 107
                                                                                                                                                                                                                             "Microsporidia, amitochondrial protists, poss protein gene of mitochondrial evolutionary or Mol. Biol. Evol. 15:683-689(1998).

-i- CATALYTIC ACTIVITY: ATP + L-tryptophan + diphosphate + L-tryptophanyl-tRNA(Trp).

-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
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                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon
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Aminoacyl-tRNA_synthetase; Protein biosynthesis; Ligase;
                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98277683;
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DR EMBL; AJ012470; CAA10034.1; -.

DR InterPro; IPR0012305; tRNA-synt_1b.

DR InterPro; IPR001412; tRNA-synt_1b; 1.

DR Pfam; PF00579; tRNA-synt_1b; 1.

DR PROSITE; PS00178; AA_TRNA_LIGASE I; 1.

KW Aminoacyl-tRNA synthetase; Protein blosynthesis; Ligase; ATP-binding. FT SITE 89

FT NON TER 134 134

SQ SEQUENCE 134 AA; 15744 MW; 60E2935B7E1E344F CRC64;

Query Match 18.2%; Score 386; DB 1; Length 134;
Best Local Similarity 51.5%; Pred. No. 5.8e-25;
Matches 68; Conservative 25; Mismatches 35; Indels 4; Gaps 1;

PROSITE 134 DEVDPWTYOTSSAK----GIDYDKLIVRFGSSKIDKELINRIERATGORPHHFIRRGIF 67

DB 3 EORITPWDVEVVSTDEVPVAIDYDKINOFGCEKFNQALADRLEKLSGKPAHYFFRRGIV 62

QY 12 EDFVDPWTVOTSDEVPVAIDYDKINOFGCEKFNQALADRLEKLSGKPAHYFFRRGIV 62

QY 68 FSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTD 127

DB 63 FAHRDFNLLLDEIANNRFFYLYTGRGPSSEXTMHIGHTIFFLLCKYMQDAFKIRLVIQITD 122

QY 128 DEKYLWKDLTLD 139

DB 123 DEKFLWKSMRLE 134

Search completed: July 10, 2003, 12:30:35

Job time: 9.74909 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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6.2	6.3	6.4	6.4	6.5	6.9	6.9	6.9	7.1	7.1	7.2	7.2	7.3	7.5	7.5	7.5
328	343	365	328	319	337	375	339	408	327	344	344	102	346	375	337
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`tryptophan-tRNA li	tryptophan-tRNA li	tryptophanyl-tRNA	 tryptophan-tRNA li 	tyrosine-tRNA liga	tryptophan-tRNA li	tyrosine-tRNA liga	tryptophan-tRNA li	probable tyrosine-	tyrosyl-tRNA synth	tryptophan-tRNA li	tryptophanyl tRNA	probable tryptopha	tryptophanyl-tRNA	tyrosyl-tRNA synth	tryptophan-tRNA li

ALI GNMENT

A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-141;182-471 <FRO1>
A;Residues: 1-141;182-471 <FRO1>
A;Residues: 1-141;182-471 <FRO1>
A;Cross-references: GB.X67918; GB.S62837; NID:g37968; GB:X67919; NID:g37969; GB:X67920; A;
NID:g37974; GB:X67925; GB:S62855; NID:g37975; GB:X67926; GB:S62856; NID:g37976; GB:X67920; A;Note: the authors translated the codon GGG for residue 55 as Cys and GAG for residue 34
A;Note: this translation is not annotated in GenBank entries HSWRSX1A, HSWRSX1B, HSWRSX2,
A;Note: this translation is not annotated in GenBank entries HSWRSX1A, HSWRSX1B, HSWRSX2,
R;Frolova, L.Y.; Sudomoina, M.A.; Grigorieva, A.Y.; Zinovieva, O.L.; Kisselev, L.L.
Gene 109, 291-296, 1991 A;Cross-references: GB:M77804; NID:g184656; PIDN:AAA67324.1; PID:g184657 R;Buwitt, U.; Flohr, T.; Boettger, E.C. EMBO J. 11, 489-496, 1992 A;Title: Molecular cloning and characterization of an interferon induced human cDNA with A;Reference number: S19246; MUID:92164636; PMID:1537332 A;Accession: S19246 A;Cross-references: GB:X59892; NID:g30820; PIDN:CAA42545.1; PID:g30821
R;Rubin, B.Y.; Anderson, S.L.; Xing, L.; Powell, R.J.; Tate, W.P.
J. Biol. Chem. 266, 24245-24248, 1991
A;Title: Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts.
A;Reference number: A41706; MUID:92105071; PMID:1761529 A;Residues: 1-423,'R',425-471 <BUW>
A;Cross-references: EMBL:K62570; NID:g32708; PIDN:CAA44450.1; PID:g32709
A;Note: 213-Ser and 214-Tyr were also found
R;Frolova, L.Y.; Grigorieva, A.Y.; Sudomoina, M.A.; Kisselev, L.L.
Gene 128, 237-245, 1993 A;Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamma A;Reference number: A41633; MUID:92107982; PMID:1763065 C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 03-Jun-2002
C;Accession: A41633; A41706; S19246; JN0676; JH0533; S26287 tryptophan-tRNA ligase (EC 6.1.1.2) [similarity] - human N, Alternate names: interferon-inducible protein IFP53; peptide-chain release A;Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response elemer A;Reference number: JN0676; MUID:93292992; PMID:7685728 A;Accession: JN0676 A; Status: preliminary A; Molecule type: mRNA A; Accession: A41706 R;Fleckner, J.; Rasmussen, H.H.; Justesen, J. Proc. Natl. Acad. Sci. U.S.A. 88, 11520-11524, 1991 A; Molecule type: mRNA A;Status: preliminary A;Residues: 1-471 <RUB> A; Residues: 1-471 <FLE> A;Molecule type: mRNA A;Status: preliminary A; Accession: A41633 factor homol

Gene 109, 291-296, 1991
A;Title: Cloning and nucleotide sequence of the structural gene encoding for human trypto
A;Reference number: JH0533; MUID:92112058; PMID:1765274
A;Accession: JH0533

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tryptophan-tRNA ligase (BC 6.1.1.2) [validated] - bovine
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Bos primigenius taurus (cattle)
C;Dates: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 03-Jun-2002
C;Accession: A40279; JN0354; $10460; $14540
R;Garret, M: Pajot, B: Trezeguet, V: Labouesse, J: Merle, M: Gandar, J.C.; Benedett Biochemistry 30, 7809-7817, 1991
A;Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic ship and the sequence number: A40279; MUID:91329348; PMID:1907847
A;Accession: A40279; MUID:91329348; PMID:1907847
A;Accession: A40279; MUID:91329348; PMID:1907847
A;Accession: A40279; MUID:91329348; PMID:1907847
A;Cross-references: GB:M74074; EMBL:X53918; NID:9163798; PIDN:AAA30799*1; PID:9163799
A;Accession: J-475 <GAR-
A;Cross-references: GB:M74074; EMBL:X53918; NID:9163798; PIDN:AAA30799*1; PID:9163799
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A;Cross-references: GB:M74074; EMBL:X53918; NID:9163798; PIDN:AAA30799*1; PID:9163799
A;Cross-references: GB:M74074; EMBL:X53918; NID:9163798; PIDN:AAA30799*1; PID:9163799
A;Cross-references: GB:M74074; EMBL:X53918; NID:9163798; PIDN:AA30799*1; PID:9163799
A;Cross-references: GB:M74074; EMBL:X53918; NID:9
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A;Cross-references: GB:M61715; NID:g340367; PIDN:AAA61298.1; PID:g340368
A;Experimental source: fibroblast
C;Genetics:
A;Gene: GB:WARS; IFP53
A;Gross-references: GBB:119632; OMIM:191050
A;Map position: 14q23-14q31
A;Cross-references: GBB:119632; OMIM:191050
A;Map position: 14q23-14q31
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase rC;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis F;19-64/Domain: amino acid-tRNA ligase repeat homology <ATL>
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Pred. No. 2e-163;
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A;Cross-references: GB:M33460
R;Frolova, L.Y.; Dalphin, M.E.; Justesen, J.; Powell, R.J.;
EMBO J. 12, 4013-4019, 1993
A;Title: Mammalian polypeptide chain release factor and try
A;Reference number: S37396; MUID:94009008; PMID:8404867
A;Recession: S37396
A;Molecule type: mRNA
A;Residues: 166-177 <FRO>
C;Genetics:
A;Genetics:
A;Gene wRS
C;Complex: homodimer [validated, MUID:94009008]
C;Punction:
A;Description: EC 6.1.1.2 [validated, MUID:94009008]; catalyzes the ATP-dependent format A;Note: mammalian WRS (tryptophanyl-tRNA synthetases) and eRF (polypeptide chain release C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase; repeat homology C;Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; metalloprotein; protein t P;23-68/Domain: amino acid-tRNA ligase repeat homology <ATL>
F;174-177/Region: ATP-binding motif (HXGH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tryptophan-tRNA ligase (EC 6.1.1.2) [validated] - rabbit
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence revision 13-Feb-1998 #text_change 03-Jun-2002
C;Accession: A35904; S37396
C;Accession: A35904; S37396
R;Lee, C.C.; Craigen, W.J.; Muzny, D.M.; Harlow, E.; Caskey, C.T.
R;Lee, C.C.; Craigen, W.J.; Muzny, D.M.; Harlow, E.; Caskey, C.T.
Proc. Natl. Acad. Sci. U.S.A. 87, 3508-3512, 1990
A;Title: Cloning and expression of a mammallan peptide chain release factor
A;Reference number: A35904; MUID:90239043; PMID:2185472
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-475 < LEE>
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Pred. No. 1.7e-157;
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Query Match Best Local

Local Similarity

92.0%;

Score 1946.5; DB 1; Pred. No. 8.2e-151; 1; Mismatches 15;

Indels Length

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Gaps

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Conservative

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A;Gene: WRS
A;Note: clone S5
A;Note: clone S5
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology C;Keywords: alternative splicing; aminoacyl-cRNA synthetase; ligase; protein biosynthesi F;1-481/Product: tryptophan-tRNA ligase alpha-2 chain long splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain splice form #status predicted F;1-475/Product: tryptophan-tR
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R;Kisselev, L.L.
Biochimie 75, 1027-1039, 1993
A;Title: Mammalian tryptophanyl-tRNA synthetases.
A;Reference number: I49391; MUID:94257729; PMID:7515282
A;Accession: I49391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tryptophan-tRNA ligase (EC 6.1.1.2) alpha-2 chain - mouse (Species: Mus muscullus (house mouse) C; Species: Nus muscullus (house mouse) C; Date: 07-May-1995 #sequence_revision 10-Nov-1995 #text_C; Accession: 550053; S50052; I49391; S31461; S31462 R; Pajot, B.; Sarger, C.; Bonnet, J.; Garret, M. J. Mol. Biol. 242, S99-603, 1994 J. Mol. Biol. 242, S99-603, 1994 A; Title: An alternative splicing modifies the C-terminal A; Reference number: S50052; MUID:95018226; PMID:7932716 A; Accession: S50053
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A;Molecule type: mRNA
A;Residues: 1-475 <PAW>
                                                                                                                                                                                                                                                                        A;Introns: 475/2
A;Note: the list of
C;Genetics: <SSF>
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A; Residues: 1-481 <RES>
A; Cross-references: EMBI
C; Genetics: <LSF>
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A;Genetics: LSF
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A; Residues: 1-481 < PAJ>
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                                                           acid-tRNA ligase repeat
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FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMT

126 123

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FFSHRDFDMILDRYEQKKPFYLYTGRGPSSDSMHLGHMIPFMFCKWLQDVFQVPLVIQLT

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RESULT 5
$58157

hypothetical protein SPAC2F7.13c - fission C;Species: Schizosaccharomyces pombe C;Ate: 13-Jan-1996 #sequence revision 01
C;Accession: S58157; T38561
R;Gentles, S.; Churcher, C.M.
submitted to the EMBL Data Library, July *.paference number: S58145
                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-395 <GE2>
A;Cross-references: EMBL:Z50142; PIDN:CAA90500.1; GSPDB:GN00066;
A;Experimental source: strain 972h-; cosmid c2F7
C;Genetics:
A;Gene: SPDB:SPAC2F7.13c
A;Map position: 1
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA
                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z50142; NID:g1052783; PIDN:CAA90500.1; R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; submitted to the EMBL Data Library, July 1995
A;Reference number: Z21799
A;Accession: T38561
                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <GEN>
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                                                                       Matches
                                                                                   Query Match
Best Local S
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                                    11
                                                                     235;
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EEDFVDPWTVQTS----SAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKIQKHVTFNQVKGIFGFTDSDCIGKSSFPAVQAAPSFSNSFPKIFRDRTDIQCLIPCAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNKHAFSGGRDTVEEHRQFGGNCEVDVSFMYLTFFLEDDDRLEQIRKDYTSGAMLTGELK
                                                                   Conservative
                                                                                                                                  tryptophan-tRNA ligase; amino acid-tRNA ligase
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                                                                  57.2%; Score 1210; DB 2; 59.6%; Pred. No. 7.2e-91; cive 60; Mismatches 91;
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21; Mismatches
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ches 16;
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A;Reference number: $66791

A;Reference number: $66791

A;Recession: $66793

A;Molecule type: DNA

A;Residues: 1-432 < DUR>
A;Gross-references: EMBL: Z74839; NID: g1419947; PII

A;Gross-references: EMBL: Z74839; NID: g1419947; PII

A;Genetics:
A;Genetics:
A;Genetics:
SGD: WRS1; WRS1; WIPS: YOL097c

A;Gross-references: SGD: S0005457

A;Map position: 15L
C;Superfamily: mammalian tryptophan-tRNA ligase; aC;Keywords: ligase
C;Keywords: ligase
F;117-120/Region: ATP-binding motif (HXGH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryptophan-tRNA ligase (EC 6.1.1.2) [similarity] - yeast (Saccharomyces N;Alternate names: protein HRE412; protein 00792; tryptophanyl-tRNA synt C;Species: Saccharomyces cerevisiae c;Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 03-Jun;2 C;Accession: S51901, S59.17; 566793 R;Vandenbol, M; Durand, P; Portetelle, D.; Hilger, F. submitted to the RMBL Data Library, January 1995 A;Description: Sequence analysis of a 44kb DNA fragment of yeast chromos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:ZA8149; NID:g663234; PIDN:CAA8816
A;Note: the nucleotide/sequence was submitted to the EMBL
R;Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
submitted to the Protein Sequence Database, July 1996
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Yeast 11, 1069-1075, 1995
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A; Residues: 1-432 < VAW>
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A;Status: nucleic acid sequence not shown; translation not
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A;Residues: 1-432 <VAN>
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Best Local S
Matches 217
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                            62
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                                                                                                                                                                                     Similarity
LRRGIFFSHRDMNQVLDAYENKKFFYLYTGRGFSSEAMHVGHLIFFIFTKWLQDVFNVPL
                                                                                            ATEAEEDFVDPWTV-----QTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHF
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                                                                                                                                                             Conservative
                                                                                                                                                                                     54.8%;
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                                                                                                                                                             71;
                                                                                                                                                                                  Score 1163; DB 2;
Pred. No. 5.6e-87;
                                                                                                                                                               Mismatches
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Library, January
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-386 <KUR>
A;Cross-references: GB:AE006641; NID:gl3813608; PIDN:AAK40778.1; GSPDB:GN00155
C;Genetics:
A;Gene: trpS
A;Gene: trpS
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat
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    365
                                                  286
                                                                                          306 AFSGGRDTIEEHROFGGNCDVDVSFMYLTFFLEDDD-KLEQIRKDYTSGAMLTGELKKAL 364
                                                                                                                                          226
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                                                                                                                                                                                  246 YFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKH 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 VIQMIDDEKYLWK-DLILDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191;
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    IEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLS 397
                                                                                                                                                                                                                                    KKLTPSEVRATPGLDASSNIGLIFYPALQIAPT-----MFEKK---RCLIPAGIDQDP
                                                                                                                                                                                                                                                            KHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDP
                                                                                                                                                                                                                                                                                                                                                    DDEKYLWK-DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                          FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPDEFTVTPWEV-----KGKVDYDKLIVQFGTQKITEELKQRIKNLAGDL-HVMLRRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEAEEDFVDPWTVQTSSAKG-IDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
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                                               AFSGGOPTIELHRKYGGNPEIDVPFQWLYYFFEEDDNRIKEIEEEYRSGKMLTGELKQIL
                                                                                                                                       YWRLQRDIAESLGYYKAAQIHSKFLPPLTGPEGKMSSSNPETAIYLVDDPKTVERKIMKY
                                                                                                                                                                                                                                                                                                                            DDEKYMRNPEFTLDQTRSWAYDNILDIIAVGFNPDKTFIFQDTEYI---RNMYPITVKIA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKLCIETLQEFVKAFQERRAQVDEETLDKFMVPHKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KINKYAFSGGQVSADLHRELGGNPDVDVAYQYLSFFKDDDVFLKECYDKYKSGELLSGEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDODÞÝFRVCRDVADKLKÝSKÞÁLLHSRFFÞÁLQGSTTKMSASDDTTAIFMTDTÞKQIQK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVRVSRQITGSTAKAVFGFNDSDCIGKFHFASIQIATAFPSSFPNVLGLPDKTPCLIPCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.9%; Score 907; DB 2; 48.6%; Pred. No. 3.6e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412
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Awayez, M. goc, H.P.;

Chan-Vider, P

360

376

256

300

196

Gaps

10

126 59 66

245

225

285

repeat

homology

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A;Molecule type: DNA
A;Residues: 1-385 <KAW>
A;Residues: 1-385 <KAW>
A;Cross-references: GB:AJ248288; GB:AL096836;
A;Experimental source: strain Orsay
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
              A; Molecule type: DNA
A; Residues: 1-301 < K
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A; Accession: C75020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tryptophanyl-tRNA synthetase (trps) PAB1111 - Pyroc C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 C;Accession: C75020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
A;Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA31046.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIQEFLKEHQKRRKKAEKQIEK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEK 130
                                                                                                                                                                                                                                                                                   VLQPLIAEHQARRKEVTDEIVK 388
                                                                                                                                                                                                                                                                                                                 GRPTLKEQREKGGEPEKCVVFKWLEIFFEEDDK--KLKERYYACKNGELTCGECKRYLIS
                                                                                                                                                                                                                                                                                                                                        GRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
                                                                                                                                                                                                                                                                                                                                                                       QRDFAESLGYYKTAAIHSKFVPSLTSLSGKNSASKPETAIYLTDSPEDVEKKVWKFALTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLFKENLTFEDTKHWAYENILDIIAVGFDPDKTFIFQNSEF----TKIYEMAIPIAKKIN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDYDKVLQDYEEGRGFFLYTGRGPSG-PMHIGHIIPFFATKWLQEKFGVNLYIQITDDEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammalian tryptophan-tRNA ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.9%; Score 803; DB 2; Length 38: 45.3%; Pred. No. 1.1e-57; ative 63; Mismatches 120; Indels
                                                                                                          M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 2; Length 385;
1.1e-57;
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                                                                                 genome of a
                                          translation
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 PID:g3258363
                                                                                                                                                        03-Jun-2002
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                                          not shown
                                                                                  hyper-thermophilic
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tryptophanyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1 (;Species: Halobacterium sp. NRC-1 (;Species: Halobacterium sp. NRC-1 (;Species: Halobacterium sp. NRC-1 (;C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 (;Accession: G84373 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; LA;Title: Genome sequence of Halobacterium species NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: G84373
                                                                                                                                                                                                                                                                                                                                                                      A;Gene: trpS2
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <STO>
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A;Note: this accession replaces an interim acce
C;Genetics:
A;Gene: PH1921
C;Superfamily: yeast tyrosine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004437; NID:g10581646; PIDN:AAG20355.1; GSPDB:GN00138 C;Genetics:
                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity 44.2
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                           141;
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                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                     HRDMNQVLDAYENKKFFYLYTGRGFSSEAMHVGHLIFFIFTKWLQDVFNVPLVIQMTDDE
                                        KYLWKDLTLDQAYGDAVE-NAKDIIACGFDINKTFIF---SDLDYM-GMSSGFYKNVVKI 184
                                                                                                                                                                                                                     AEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPDKTFIFONSEF----TKIYEMAIPIAKKINFSMAKAVFGFTEQSKIGMIFFPAIQIAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAP
KYWFKDQTPAET-GDYLRANLRDLLAVGFDPELTRIVVDTRDADVLYPLATAFAGDV----
                                                                                                                                                                                         ADGNOVTPYAVESDD----LDYEKLLARFGADELTDDQRARFP-----DHPLVNRGLFYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLS 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKMSASKPETAIYLTDSPEDVEKKVWKFTLTGGRPTLKEQREKGGEPEKCVVFKWLEIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TF-----FERK---RCLIPAAIDODPYWRLQRDFAESLGYYKTAALHSKFVPSLTSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEDDK--KLKERYYACKNGELTCGECKRYLISKIQEFLKEHQRRRKK-AEKLVEKFKYTG
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.6%; Score 626.5; DB 2
44.2%; Pred. No. 1.9e-43;
ative 56; Mismatches 92
                                                                                                                                                                                                                                                                                   25.3%; Score 534.5; DB 2
35.4%; Pred. No. 8.3e-36;
tive 76; Mismatches 140
                                                                                            -IVTGVGPSG-PMHLGHAMVFYFARRLQDEFGARVYVPLSDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an interim accession for a sequence replaced
                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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tryptophan-tRNA ligase (EC 6.1.1.2) - Methanococcus jannaschii

N;Alternate names: tryptophanyl-tRNA synthetase
(;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #text_change 03-Jun-2002
C;Accession: F64476
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Reinth, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64476
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-370 <BUL>
A;Cross-references: GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99425.1; PID:g1592065; TC;Genetics:
A;Map position: FOR137585-1376997
A;Start codon: GTG
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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Best Local Similarity
                         364 LIEVLOPLIAEHQARRKEVTDEIVK 388
                                                                                                                  307
                                                                                                                                                                                                                                                        168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 DLAADRITEFLAAHQRRRAALGD--VTEALDAFRLTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185
                                                                                                                                                                                                                                                                                                                                                                                         134 KDLTLDQAYGDAV-ENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKI-QKHVTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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                                                                                                FSGGRDTIEEHRQFGG---NCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKA 363
                                                                                                                                                                                                  TRDVAPR---IGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHA
                                                                                                                                                                                                                                                     EMKAIYGFKGETNIGHVFAPIVQVADIL---HPQLDENLSPEPKPVVVPVGIDQDPHIRL
                                                                                                                                                                                                                                                                             RNMSFETTKELALNEYITNYIALGLDPEKINVYLQSKYQKV-----KDLALILSKRTNWS
                                                                                                                                                                                                                                                                                                                                                                                                                                       VDAIKNNKEFAVVSGMMPSGK-MHFGHKMVVDLLKFYQKYTDNINIPI----ADLEAYWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQ---DVFNVPLVIQMTDDEKYLW 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KALIEVLOPLIAEHOARRKEVTDEIVKEFMTPRKLSFD
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                                                                        KTGGRETLEEHKKYGGVPEECVVYELFLY--HLILDDKELAEIYQKCRSGELTCGKCKKM
                                                                                                                                                                 TRDIANRAKEFKFIPPSSTYHRFMTGLLGG--KMSSSKPETAIFLTDDEKTVKKKIFS-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PW--ETPAV--IDYKKIMEQFGVKPIVDVLGDLKEE-----HHFFRRNIILGHRDFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.4%; Score 409.5; DB 2; 30.9%; Pred. No. 1.3e-25; tive 72; Mismatches 153;
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tryptophan-tRNA ligase (EC 6.1.1.2) [imported] - Encephalitozoon CySpecies: Encephalitozoon cuniculi C;Species: Encephalitozoon cuniculi C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change C;Accession: T43806 R;Peyretaillade, E.; Broussolle, V.; Peyret, P.; Metenier, G.; G Mol. Biol. Evol. 15, 683-689, 1998 Mol. Biol. Evol. 15, 683-689, 1998 A;Title: Microsporidia, amitochondrial protists, possess a 70-kD A;Reference number: 222693; MUID:98277683; PMID:9615449 A;Accession: T43806 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                RESULT
T43806
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Best Local S
Matches 107
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tryptophan-tRNA ligase (EC 6.1.1.2) - Methanobacterium thermoautotrophicum (strain Delta N,Alternate names: tryptophanyl-tRNA synthetase C;ppecies: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jun-2002 C;Accession: E69131
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C; Lee, H.; Dubois, J.; Aldredge, T.; E; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi A;Reference number: A69000; MUID:98037514; pMID:9371463
A;Accession: E69131
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Cross-references: GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB84757.1; PID:g2621301
A;Experimental source: strain Delta H
C;Genetics: MTH251
A;Gene: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 DLTLDQAYGDAVEN-AKDIIACGFDINK------TFIFSDLDYMGMSSGFYKNVVK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 RIISAMKKGEDFAVVTGMMPSGR-MHIGHKMIVDQLRW-YDRMGAEIFIPIADMEAYSAR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 QVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVDFEDSRRIAIEEYIAGYIALGLDLEKDNIHVYLQSENLMVEDLAYV------
                                                                                                                                                                                AKI-RNAKTGGRETLKEQRELGGVPEECIIYETLLYHMSGSDSRLEEIYESCRNGTLMCG
                                                                                                                                                                                                                                                                      TKVNKHAFSGGRDTIEEHROFGGNCDVDVSFMYLTFFLE-DDDKLEQIRKDYTSGAMLTG
                                                                                                                                                                                                                                                                                                                                                                 DPHIRLTRDIAARFRDRYGFILPSSTYHRFMGGLTGG--KMSSNRPKSAIFLSDTPEEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                        DPYFRMTRDVAPRI----GYPKPALLHSTPFPALQGAQTKMSASDPNSSIFLTDTAKQIK 299
                                                                                     ELKKALIEVLOPLIAEHQARRKE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAGKVNENELRAIYGFTGSTSMAHMYAPIIQVSDILHPQLDELGGPR---PVIVPVGPDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQ
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ECKNNTAEFIRKFFEELSVKREK 353
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Pred. No. 1.2e-24
6; Mismatches 15
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Encephalitozoon cuniculi (fragment)

70-kDa heat shock protein gene Gouy, M.; Vivares,

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RESULT 14
E69461
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.

Smith, H.O.; Woese, C.R.; Venter, J.C.

Smith: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A; Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: E69461
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A;Residues: 1-134 <PBY>
A;Residues: 1-134 <PBY>
A;Cross-references: EMBL:AJ012470; PIDN:CAA10034.1
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-420 <KLE>
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
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Best Local
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311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th . 17.5%; Score 370.5; DB 2
Similarity 27.3%; Pred. No. 2.3e-22;
.18; Conservative 60; Mismatches 166
                                                                                                                                                                                                                                                                                                                                                              DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVV-KIQKHVTFNQV 193
                                                                                                                                                                                                                              RAIYGFNSDTSLAKMFVTAIQAADIL---HPQLSDFGGPKPVVVPVGADQDPHMRLTRDL
                                                                                                                                                                                                                                                                                                                         GLSWEKTRELGMLYIKSIIALGLREDAVIYFQS-----KSSHVKDLAFELSAEVNFSEL
                                                                                                                                                                                                                                                                                                                                                                                                                RIIEAMQKKEPWAVMSGFMPSG-LPHFGHKWTMDEIVWHQSAGGKAFV-AIADMEAHSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEKFLWKSMRLE 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAHRDFNLLLDEIANNRPFYLYTGRGPSSKTMHIGHTIPFLLCKYMQDAFKIRLVIQITD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDFVDPWTVQTSSAK----GIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIF
RDTIEEHRQFGGNCDVDVSFMYLTFFLED-DDKLEQIRKDYTSGAMLTGELKKALIEVLQ 369
                                             EVEIGGFAFIPPSSTYHRFTTGLTGG--KMSSSKPESYISLLDPPEEGAKKVMK-AFTGG
                                                                                                                                                                                     APRI ----
                                                                                                                                                                                                                                                                       KGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDV
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                                                                                                                                       AARISIFSFEPVEGGVRVRSRKGAEYLSSLRDLEFDKKIYEEHMDIFGEAEEIERAVRKI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTPWEVEGV----IDYSKLIEEFGMQPF-SEVLPEID----NPHILMRRGAIFGHRDYW
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                                                                                      -GYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGG 310
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Pred. No. 2.5e-24;
5; Mismatches 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166;
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: D72477
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A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81476.1;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 KDLTLDQAYGDAYEN-AKDIJACGFDINKT-FIFSDLDYMGMSSGFYKNVVKIQKHVTFN 191
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                                                                                  ALIEVLOPLIAEHOARRKEVTDEIVKEFMTPR 394
                                                                                                                                                                         LTGGRATAEEQRRLGGVPEVCSVYHMDLYHLMPDDGEVKHI - -
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1: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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9 US-09-919-039-163
9 US-09-913-718-16
9 US-09-925-302-855
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                                         Sequence 14, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 163, App
Sequence 558, App
Sequence 8545, Ap
Sequence 8545, Ap
Sequence 3545, Ap
Sequence 45, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 57, App
Sequence 57, App
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45	44	43	42	41	40	39	38	37	36	35	34	33	3 2	31	30	29	28	27	26	25	24	23	22	21	20
105	105.5	106	106	106.5	107	107	108	108	108	108	108	108	108	110.5	112	113	113	113.5	120	128	132.5	132.5	134	142.5	146
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Sequence 43, Appl		Sequence 45, Appl	Sequence 45, Appl	Sequence 10371, A	Sequence 51, Appl	Sequence 51, Appl	Sequence 13806, A	Sequence 64, Appl	Sequence 59, Appl	50,		Sequence 59, Appl	Sequence 50, Appl	Sequence 12259, A	Sequence 4252, Ap	Sequence 12649, A	Sequence 5494, Ap	Sequence 10678, A	Sequence 52, Appl	Sequence 11070, A	Sequence 2, Appli	Sequence 4, Appli	Sequence 8, Appli	Sequence 10954, A	Sequence 11422, A

ALIGNMENTS

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; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: supermini TrpRS in pET20B
US-09-813-718-14
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Publication No. US20020182666A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: The Regulation of Anglogenesis
FILE REFERENCE: 00-221
FILE REFERENCE: 00-221
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CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 401; Conservative
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                              Match 100.0%; Score 2116; DB 9; Local Similarity 100.0%; Pred. No. 5.7e-192;
182
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                    VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                   LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                        LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
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US-09-813-718-51 US-10-128-714-3379 US-10-128-714-8379

Sequence 51, Appl Sequence 3379, Ap Sequence 8379, Ap

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RESULT 2
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US-09-813-718-12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human Aminoacyl-trnA Synthetase Polypeptides Useful For FILE OF INVENTION: The Regulation of Angiogenesis FILE REFERENCE: 00-221 CURRENT APPLICATION NUMBER: US/09/813,718 CURRENT FILING DATE: 2001-03-21 NUMBER OF SEQ ID NOS: 58 SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Wakasugi, Kei
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
                                                                                   KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
                                                                                                                                               IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                                                                                                                                                           VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                             VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSSFPQIFRDRTDIQCLIPCA
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                                                               KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
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KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
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Pred. No. 6.1e-192;
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RESULT 3 US-10-126-467B-2

Sequence

2

Application US/10126467B

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APPLICANT: Paley, Elena
TITLE OF INVENTION: ANIMAL MODEL OF AND TEST FOR ALZHEIMER'S DISEASE
FILE REFERENCE: PALL-111
CURRENT APPLICATION NUMBER: US/10/126,467B
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/284,980
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: 09/513,895
PRIOR APPLICATION NUMBER: 09/513,895
PRIOR APPLICATION NUMBER: 09/384,869
PRIOR APPLICATION NUMBER: 09/384,869
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 471
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; ORGANISM: Homo sapiens
US-10-126-467B-2
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                                                                      APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT PILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09813718 Publication No. US20020182666A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication No. US20030059797A1 GENERAL INFORMATION:
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Best Local Similarity
                 TYPE: PRT ORGANISM: Artificial Sequence
FEATURE:
                                                         LENGTH:
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Pred. No. 6.8
0; Mismatches
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RESULT 5
US-09-919-039-163
; Sequence 163, Application US/09919039
; Publication No. US20030108871A1
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APPLICANT: KASEY, MATCHEW R.
APPLICANT: KASEY, MATCHEW R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 163
LENGTH: 471
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                                                                                                                                                                                                                                                  -09-919-039-163
                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 2705515CD1
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                           Local Similarity
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LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
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                                                                                                    SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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Pred. No. 1.8e-190;
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Pred. No. 7.1e-192;
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PRIOR FILING DATE: 2000-03-08
PRIOR PRIOR TILING DATE: 1909-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 558
TENDOTH: 475
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; ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA104
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CURRENT FILING DATE: 2001-08-10
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435
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Similarity 99.5%;
99; Conservative
                                                                                                                                                                                                                             VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
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                    KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ. 401
                                                                                                                                                           IDQDFYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTXMSASDPNSSIFLTDTAKQIKT 300
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KKALIEVLOPLIAEHQARRKEVIDEIVKEFMIPRKLSFDFQ 475
                                                                   KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
                                                                                                   KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
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                                                                                                                                       IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
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Pred. No. 1.8e-190;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: human minor
; OTHER INFORMATION: TrpRS fragment in pET20B
US-09-813-718-16
                                                                                                                                                                                                                                                                                                                           RESULT 8
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Publication No. US20020182666A1

GENERAL INFORMATION:

APPLICANT: Schimmel, Paul

APPLICANT: Wakasugi, Keisuke

TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful

TITLE OF INVENTION: The Regulation of Angiogenesis
                                                                                                                                                                                                                                                   Sequence 8545, Application US/10128714 Publication No. US20030119013A1
                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity
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              APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lenshkin, Alexey M
APPLICANT: Lenshkin, Alexey M
APPLICANT: Lensheux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Methods of Use
TITLE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 00-221
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APPLICATION NUMBER: US/10/128,714
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Pred. No. 6.9e-180;
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PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/316,362
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 8545
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                                                                                                                                       297 QIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAML
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                                                                                                                                                                                                                                                                                                                                                                                                                       122 VIQMTDDEKYLW-KDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
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                                                                                         RIKNKINKYAFSGGODTAELORÓLGANTKODVPFQYLTFFMEDDEELERIRVAYEKGEML
                                              TGELKKALIEVLOPLIAEHOARRKEVTDEIVKEFMTPRKLSF 398
                                                                                                                                                                                                                               IPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAK 296
                                                                                                                                                                                                                                                                             ICRMAKRITINSVRGTFGFNDSNNVGEFHFCATQSATAFATSFPHIFGTDRKKVSSIPCL
TGEVKQKCIAELQAYVQAFQERRAQVTDEIVAEFMRPRSLEW 421
                                                                                                                                                                                      IPCAIDQDPYFRQCREHAEKMKYKKPSLIHAIFLPALQGPGSKMSASVETSAIFMNDAPN 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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RESULT 9

US-09-925-302-855

Sequence 855, Application US/09925302

Patent No. US20020044941A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Ant
FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 855

LENGTH: 173

TYPE: PRI

ORGANISM: Homo sapiens
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142 VIMLTDDE 149

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PRIOR FILLING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILLING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILLING DATE: 2001-06-05
PRIOR FILLING DATE: 2001-06-05
PRIOR FILLING DATE: 2001-07-09
PRIOR FILLING DATE: 2001-09-31
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILLING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 3545
LENGTH: 179
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                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
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OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (168)
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122 VIQMTDDE 129
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                                                                                    62 LRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPL 121
                                                    82 MRRGIVFSHRDLNLILDRYEKGQPFYLYTGRGPSSDSMHVGHTIPFEFTKWLQDVFDCPL 141
                                                                                                                             22
                                                                                                                                                                                                       76;
                                                                                                                                                          ATEAEEDFVDPWTV-----QTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYSYAVENAKDIIACGFDINKTFIFS
                                                                                                                               ASKAVAQVVTPFDVSGGVDESGKLLPVDYDKLVREFGATRISKELLERFERVTGRRPHRF
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                                                                                                                                                                                                 19.6%; Score 414.5; DB 9 59.4%; Pred. No. 2.3e-31; tive 20; Mismatches 27
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Pred. No. 7.9e-71;
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RESULT 13
US-09-613-718-48
; Sequence 48, Application US/09813718
; Publication No. US20020182666A1
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US-09-813-718-45
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APPLICANT: Schimmel, Paul
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 85
TYPE: PRT
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Publication No. US20020182666A1
GENERAL INFORMATION:
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SEQ ID NO 45
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Best Local Similarity
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APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 3.2e-20;
2; Mismatches 4
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GENERAL INFORMATION:

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RESULT 15
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US-09-813-718-47
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US-09-813-718-47
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LENGTH: 85
TYPE: PRT
                                                                                                        Sequence 557, Application US/09925302 Patent No. US20020044941A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48
LENGTH: 85
TYPE: PRT
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Publication No. US20020182666A1
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               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For TITLE OF INVENTION: The Regulation of Angiogenesis FILE REFERENCE: 00-221
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APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
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52; Conserv
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85.2%;
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Pred. No. 1.8e-18;
6; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                            Score 263; DB 9; Length 85; Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Search completed: July 10, Job time : 21.4145 secs

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SEQ ID NO 557
LENGTH: 142
                                                                                                                             Matches
                                                                                                                                            Query Match
Best Local :
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 896
                                                                                                                                                                                                                                    LOCATION: (137)
OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                  LOCATION: (130)
OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (122)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
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OTHER INFORMATION:
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134 --GQGXFF 139
                             61 FLRRGIFF 68
                                                              75 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSXNXQELLXDXE-STAKXTHS 133
                                                                                    1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
                                                                                                                            Similarity 70.
48; Conservative
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Pred. No. 1.1
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        104.5
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 2000000000
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-425-666-2
US-08-743-130A-39
US-08-743-130A-2
US-08-743-130A-2
US-08-75-688-4
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US-08-415-593-4
US-09-157-257-8
US-09-157-257-8
US-09-157-257-8
US-09-157-257-8
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US-08-465-995A-4
US-08-465-995A-4
US-08-66-145-4
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88 4.2 606 3 US-09-204-764-3 87.5 4.1 855 4 US-08-890-865A-10 87.5 4.1 898 1 US-08-465-995A-2 87.5 4.1 898 2 US-08-465-994C-2 87.5 4.1 898 2 US-08-465-994C-2 87.5 4.1 898 2 US-08-101-593-2 87.6 4.1 898 2 US-08-101-593-2 87.7 4.1 898 2 US-08-101-593-2 87.8 4.1 898 2 US-08-134-001C-4511 88.6.5 4.1 849 4 US-09-134-001C-5314 88.6.5 4.1 849 4 US-09-134-001C-5314 88.6.5 4.0 410 4 US-09-134-001C-5314 88.6.5 4.0 410 4 US-09-137-257-6 88.5 4.0 410 4 US-09-137-257-6 88.5 3.9 428 3 US-08-331-625A-43 88.5 3.9 428 4 US-09-44-151-43 88.5 3.9 510 1 US-08-249-112-3 88.3.5 3.9 970 1 US-08-375-709-7 88.3.5 3.9 970 1 US-08-752-929-7
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
7 M 4 H 7 M 4 H 4 M 4 H 10 H H H
US-09-004-764-3 US-08-890-865A-10 US-08-890-865A-10 US-08-865-995A-2 US-08-465-994C-2 US-08-966-145-2 US-09-134-001C-4511 US-09-157-257-4 US-09-157-257-6 US-09-157-257-6 US-09-157-257-6 US-09-157-257-6 US-09-31-625A-43 US-08-31-625A-43 US-08-31-625A-3 US-08-349-112-3 PCT-US95-06556-3 US-08-3752-929-7

ALIGNMENTS

RESULT 1 US-08-876-885-26

Sequence 26, Application US/08876885 Patent No. 6174713

GENERAL INFORMATION:
APPLICANT: Shen, Xiaoyu

APPLICANT:
APPLICANT:

APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA CYTOPLASMIC TRYPTOPHANYL-tRNA
TITLE OF INVENTION: SYMTHETASE PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING
TITLE OF INVENTION: SAME
NUMBER OF SEQUENCES: 26

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                                                                                                                      US-08-876-885-26
                                                Matches
                                                                Query Match
Best Local &
                                                                                                                                                                                          TELEFAX: (781) 861-954
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acid
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version :
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,885
FILING DATE: 16-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hamilton, Brook STREET: Two Militia Drive
                                                                                                                                           TOPOLOGY:
                                                226;
                                                                 Similarity
TEABEDFVDPWTVQ----TSSAKGIDYDKLIVRFGSSKIDKELINRIBRATGQRPHHFLR 63
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                                                                                                                                                                                            424 amino acids
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                                                                                                                                                                                                                                               (781) 861-9540
                                                Conservative
                                                                                                                                         linear
                                               57.6%; Score 1218.5; DB 4
57.1%; Pred. No. 3.7e-128;
tive 71; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brook, Smith & Reynolds, P.C.
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                                                                               Length
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GENERAL INFORMATION:
 Best Local Similarity
                  Query Match
                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 341 amino acid
                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                         NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/928,100 FILING DATE: 12-SEP-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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ZIP: 19406-0939
                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLICANT: Greenwood, Claire
PLICANT: Lawlor, Elizabeth
TLE OF INVENTION: No. 6046174el trpS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 ECITVLQEFVSAYQERRSKVDDQVVEKFMKPHKLVF 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 ALIEVLOPLIAEHOARRKEVTDEIVKEFMTPRKLSF 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 QDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 RTSRQITTSTAKAVFGFTDSDCIGKIHFASIQIATAFPSSFFDVLGLPPKTPCLIFCAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 KIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 ELTDDEKFLFKHQLTIDDVKGFAAENAKDIIAVGFNPENTFIFSDLQYMG--GAFYENVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 QMTDDEKYLWK-DLTLDQAYGDAVENAKDIJACGFDINKTFIFSDLDYMGMSSGFYKNVV
                                                                                                                      amino acid
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Score 185.5; DB 3
Pred. No. 3.2e-12;
                Length 341;
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                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                           TELEPHONE:
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349 DYTSGAMLTGELKKALIEVLOPLIAEHQARRKEVTDEI 386
                                                                                                                                                                                                                                                                      157 PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKWSKS-LNNGIY 212
                                                                                                                                                                                                                                                                                                                                                                                                             110 NPTVKTEISQKGFGESIPTGFLVYPIAQAADITAFKANY---
269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 HVTFNQVKGIFGFTDSDCIGKISFPAIQAA--PSFSNSFPQIFRDRTDIQCLIPCAIDQD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 GDAVEN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 TDHAKDPQTIVESIGNVALDYLÄVGLDPNKSTIFIQSQIPELAELSMYYMNLVSLARLER 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKY-LWKDLTLDQAY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KPIIL-TGDRPTGK-LHIGHYVGSLKNR----
                                                                                                                                                                                               LTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDDDKLEQIRK 348
                                                                                                                                   LADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDAQEIADMKE
                                                                                                                                                                                                                                                                                                                                   PYERMTRD------VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AKDIIACGFDINKTFIF--SDLDYMGMSSGFYKNVV---KIQK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VLLQEEDKYDMFVFLADQQAL
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 341 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COFFMANTING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFFLICANT: Lawlor, Elizabeth TITLE OF INVENTION: No. 6346. NUMBER OF SEQUENCES: 6
                                                                                                                                                                                               NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,581
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Greenwood,
                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: 9619
FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                         amino acid
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                                                                          341 amino acids
                                                                                                                                                            : 610-270-4478
610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gentry, Danile
protein
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RESULT 4
US-09-425-666-2
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                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 9316
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gentry, Danile
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6416976el
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                              TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                              ENGTH:
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            1: 341 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDAQEIADMKE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKŃSKŚ-LNNGIY 212
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                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
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24.0%; Pred. No. 3.2e-12;
                                                                                                                                                                                                                                                                     08/928,100
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                                                                       N:
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; MOLECULE TYPE:
US-09-425-666-2
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Patent No.
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Best Local Similarity
            TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
                                                                 REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA TYROSYL-CRNA SYNTHETASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 01-NOV CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      Lexington
Massachusetts
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Gallant, Paul
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24.0%; Pred. No. 3.2e-12;
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                                                                                                                                                                                                                                                                   Version
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quence 2, Application US/08743130A
tent No. 5871987
                                                                                                 SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/743,130A
FILLING DATE: 01-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: CANDIDA TYROSYL-TRNA SYNTHETASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING
NUMBER OF SEQUENCES: 41
                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
  TELECOMMUNICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
                   NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP
                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 CDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALI----EVLQPLIAEHQARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 EEPKVVKKKVNSAYCAPGELKDNGLIAFIEYVIQPIAELKTGVEGAFKLDIDRPEKYGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 DTAKQIKTKVNKHAFSGG--RDT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VDAQFG-GVDQRKIFVLAEENLPSIGYKKRAHLMNPMVPGL-GQGGKMSASDPNSKIDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 IQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLT 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 NVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
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                                                                                                                                                                                                                                                                                             02173
                                                                                                                                                                                                                                                                                                                                                          Lexington
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Tao, Jianshi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallant, Paul L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sassanfar, Mandana
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                                                                                                                                                                                                                                                                                                                                                                                               Hamilton, Brook,
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INFORMATION
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20.7%;
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                       CPI95-12
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                                                                                                                                                                                                                                                                                                                                                                                                 Smith & Reynolds,
                                                                                                                                                                                         Version
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Au-Young,
APPLICANT: Murry, Lyr
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705
FILING DATE: Filed Herewith
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
             ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                        ZIP: 94304
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                                                                                                                                                                                                                                                              CITY: Palo Alto
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 YKNVVK----IQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTD 232
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                                                                                                                                                                                                                                                                                 B: Incyte Pharmaceuticals,
3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                          Au-Young, Janice
Murry, Lynn E.
IVENTION: NOVEL MONOCYTE ACTIVATING
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Coleman, Roger
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20.7%; Pred. No. 1.7e-09;
                                                                      US/08/705,868
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US-09-123-615-4
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09123615 Patent No. 6090377
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF
 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ Version 1.5
                                                                                                                                                    STREET: 3174 Po:
CITY: Palo Alto
STATE: CA
                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QARRKEVIDEIVKEFMTP--RKLS 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LDEEYLKV-----DAQF---GGIDQRKIFTFAEKYLPALGYSKRVHLMNPMVPGLTG- 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKLKFIKGTDYQLSKEYTLDVYRLSSVVTQHDSKKAGAEVVKQVEHPLLSGLLYPGLQA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDAPSPEEKLH------LITRNLQEVLGEEKLKEILKERELKIYWGTATTGKPHVAYFV 54
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                                                                                                                                                                                       3174 Porter Drive
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                                                                                                                                                                                                         Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415-855-0555
                                                                          Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DPIREKFNTPALKKLA 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------FTDSD------CIGKISFPAIQAA 216
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; CLONE: 1184699
US-09-123-615-4
                                                                                                                                                                                                                                                             US-08-855-910-11
                                                                                                                                                                                                                                                                               RESULT 9
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                                                                                                                                                                                                                Sequence 11, Approx. No. 6221640
                                                                                                                                                                                                 Patent No. 6221640
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.3%; Score 132.5; DB 3; Best Local Similarity 20.8%; Pred. No. 3.6e-06; Matches 80; Conservative 58; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                 APPLICANT:
APPLICANT:
TITLE OF INV
                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                           APPLICANT:
                                                                                                                              APPLICANT:
                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 PMSKIADFLKAGCEV--TILFADLHAYLDNMKAPWELLELRVSYYENVIKAMLESIGVPL 112
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                                                                                                                                                                                                                                                                                                                                                                                                              RDEKWGGN-----KTYTAYVD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRGPS-SEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDE--KYLWKDLTLDQ---AYGD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LDEEYLKV-----DAQF---GGIDQRKIFTFAEXYLPALGYSKRVHLMNPMVPGLTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SKMSSSEEESKIDLLDRKEDVKKKLKK-AFCEPGNVENNGVLSFIKHVLFPLKSEFVIL
                                                                                                                                                                                                                                          Application US/08855910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 amino acids
                                                                  Avruch, Anthony S.
Yu, Russell V.
Nair, Shamila
                                                                                                                                            Sassanfar, Mandana
Gallant, Paul L.
                                                                                                                              Shen, Xiaoyu
                                                                                                                                                                                   Tao, Jianshi
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               ENTEROCOCCAL AMINOACYL-tRNA SYNTHETASE
PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
71
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                                                                                                                                       US-09-352-990-28
                                                                                                                                                      RESULT 10
                                                                               Patent No. 6255090
GENERAL INFORMATION:
                                                                                                 Sequence 28, Application US/09352990 Patent No. 6255090
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       APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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STREET: Two Militia
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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REFERENCE: BB-1191
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                                                                                                                                                                                                                                                                                                            302 VNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361
                                                                                                                                                                                                                                                                                                                                                                                 242 DODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTK 301
                                                                                                                                                                                                                                                                                                                                                                                                                     208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 AVQHNVDSLSNQMKKLFGKDAEVIMVNNYDWLSELSLLDFLRDYGKNFNVNTMLAKDIVA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 LYCGVDPTGDSMHIGHLIPFMMMKRFQLAGHHPYILIGGGTGTIGDPSGRTTERVLQTME 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 LYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVI------
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                                                                                                                                                                                                                                           KALIEVLQ----PLIAEHQARRKEVTDEIVKEFMTPRK 395
                                                                                                                                                                                                                                                                             PGKR--EAQRRLAEE----
                                                                                                                                                                                                                                                                                                                                                                                                                     GPEAKVFGLTIPLMLKADGTKFGKTAGGAIWLDPKKTSPFEFYQFWLNQDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IFGFT-----DSDCIGKISFPAIQAAPSFSNSFP--QIFRDRTDIQCLIPCAI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S--RLESGISFTEFTYQILQSIDFY---TLHKKHNIQLQIGGADQWGNITAGLDLIRKKE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 amino acids
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Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.4%; Score 113.5; ilarity 20.5%; Pred. No. 0.0 Conservative 47; Mismatches
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ches 112;
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FILING DALL.

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9619072.3

APPLICATION TAME: 12-SEP-1996
                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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US-08-923-867-2
                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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                                                                                                                                                                                                                                                                             Patent No. 5851809
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Sequence 2, Apprin
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SEQ ID NO 28
LENGTH: 377
TYPE: PRT
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CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,866
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 29
                                       ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
                                                                                                                                                                                                                        TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                  COUNTRY:
ZIP: 194
COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 L-LHSTFFPALQGAQTKMSASDPN--SSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 SNSFPQIFRDRTDIQCL----IPCAIDQDPYFRMTRDV------APRIGYPKPA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 WLINCVTPLNWLERMIQFKEKAVKQGENVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 DEKYLWKDL-----TLDQAYGDAVENAKDIIACGFDINKTFIF-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 FSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 DNFFCVVDLHAITVPHNPQTLAQ---DTLTIAALYLACGIDLQYSTIFVQSHVAAHSELA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 FAHRSTTAM-----DKPRIL-SGVQPTGN-LHLGNYLGAI-RSWVEQ------QQHY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKAL--
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                                                                                                                          PΑ
                                                                                                                                                                                                                                                                                                                         Application US/08923867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRKEGARVMSLADGTKKMSKSDESELSRINLLDPPEMIKKKVKK--
                                                                                                                                                                                                                                                                  Lawlor,
                                                                                                       USA
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                  IBM Compatible
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                                                                                                                                                                                                                                             Elizabeth
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21.0%; Pred. No. 0.0015;
tive 49; Mismatches 116
                                                                                                                                                                                  Beecham Corporation
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                                                                                                                                                                                                                                               TRYPTOPHANYL CRNA
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SOFTWARE: FastSEQ for Windows Version

2.0

US/08/923,867

REFERENCE/DOCKET NUMBER: REGISTRATION NUMBER:

Edward R

38,891

P31624

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RESULT 12
US-08-928-100-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,100
FILING DATE: 12-SEP-1997
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 427
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9619072.3
FILING.DATE: 12-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                              NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Lawlor, Elizabeth
ITLE OF INVENTION: No. 6046174el trpS
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nes 42; Conserv
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                                                                                  TELEX:
                                                                                                                    TELEFAX:
                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDD 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPVGTDQKPMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSK 61
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                                      4:
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Patent No. 6165759
GENERAL INFORMATION:
                                  Query Match
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                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                            NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lawlor, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                    MOLECULE TYPE:
   Local Similarity
nes 42; Conserv
                                                                                                                                                                                                   TELEPHONE: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Dis)
COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 25.3%; nes 42; Conservative
                                                                                                       TOPOLOGY:
                                                                                                                  STRANDEDNESS:
                                                                                                                                   TYPE: amino acid
                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 DKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 IPCAIDQDPYFRMTRD-------VAPRIGYPKPALLHSTFFPALQGAQTKMSA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VPVGTDOKPMIEOTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-LNNGIYLADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA
                                                                                                                                                 197 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawlor, Elizabeth
                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                    610-270-4478
                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                     04-SEP-1997
                                                                                                                   single
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                 5.1%; Score 108; DB 4; Length 197; 25.3%; Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.1%; Score 108; DB 3;
25.3%; Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                                                                      9619072.3
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27;
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
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                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gimmi, Edward R. REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 709 of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/928 FILING DATE: 12-SEP-1997 APPLICATION NUMBER: 9619072.3
                                                                                                                                              Local
                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                             283 SDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDD 340
                                                                                              237 IPCAIDQDPYFRMTRD-----
62
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S-LNNGIYLADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDA 116
                                                             VPVGTDQKPMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE -- RAGRLPGLDG-NAKMSK
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Lawlor, Elizabeth
                                                                                                                                                                                                                                                                              197 amino acids
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                                                                                                                              Conservative
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                                                                                                                                              25.3%;
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                                                                                                                              27;
                                                                                                                           Score 108; Db 4; ... Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                                                                                                               P31624-1
                                                                                              ----VAPRIGYPKPALLHSTFFPALQGAQTKMSA 282
                                                                                                                                                             DB 4; Length 197;
                                                                                                                              Indels
                                                                                                                              24,
                                                                                                                             Gaps
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US-09-425-666-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4
Patent No.
                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6416
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19406-0939
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                                                                                                                                                                                                                                                                                                                                                ENGTH:
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117
                               341 DKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 386
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                                                                                                  283 SDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDD 340
                                                                                                                                                                237 IPCAIDODPYFRMTRD-----
                                                                 62 S-LNNGIYLADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDA 116
                                                                                                                                   5 VPVGTDQKPMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSK 61
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6416976
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QBIADMKERYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 162
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                                                                                                                                                                                                              Score 108; DB 4;
Pred. No. 0.00067;
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                -----VAPRIGYPKPALLHSTFFPALQGAQTKMSA 282
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Search completed: July 10, 2003, 12:32:51 Job time: 13.1515 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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A Geneseq 101002:*

| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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										Result No.
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94.0	94.0	99.1	99.3	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
392	392	471	475	484	484	437	437	415	415	Query Match Length
23	22	20	21	23	22	23	22	23	22	B.B.
AAE13494	AAB47618	AAY05372	AAB58220	AAE13491	AAB47615	AAE13492	AAB47616	AAE13493	AAB47617	ID
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Arabidopsis thatia Human tyrosyl-tRNA	Arabidopsis thalia	Listeria monocytog	Haemophilus influe		Human full length					Drosophila melanog	Arabidopsis thalia		Human tryptophanyl	·	Putative P. abyssi	Protein involved i	C. albicans tyrosy	C. albicans tyrosy	Lactococcus lactis	Streptococcus poly	Streptococcus pneu	Tryptophanyl tRNA	Streptococcus poly	Lung cancer associ	n	Putative P. abyssi	Lung cancer associ	Arabidopsis thalia	Tryptophanyl-tRNA		Arabidopsis thalia		Drosophila melanog

ALIGNMENTS

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RESULT 1
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WPI; 2001-626377/72.
N-PSDB; AAH43604.
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                                                                                                                                              Schimmel P,
                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-193471P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryptophanyl-tRNA synthetase; trpRS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human supermini TrpRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001WO-US08966
                                                                                                                                                                                                                                         (SCRI ) SCRIPPS RES INST
                                                                                                                                         Wakasugi K;
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RESULT 2
AAE13493
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA synthesase polypeptides or polynucleotides directly to the lumen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain; and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction -
Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                       Human supermini tryptophanyl t-RNA synthetase in pET20B
                                                                                                                 12-FEB-2002
                                                                                                                                                                                                                             AAE13493 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                     KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
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TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability;
                                                                                                                                                                                                                                                                           rheumatoid arthritis; psoriasis;
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Homo sapiens

WO200175078-AJ

11-OCT-2001

21-MAR-2001; 2001WO-US08975.

31-MAR-2000; 2000US-193471P

(SCRI) SCRIPPS RES INST

Schimmel P, ~

2002-010784/01

Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in

Example 1; Page 129-130; 149pp; English

CC truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann CC fold nucleotide binding domain and polynucleotides encoding them. The CC invention also relates to tyrosyl t-RNA synthetases (TyrRS). TrpRS CC sequences are useful for regulating vascular endothelial cell function, CC preferably angiogenesis. Angiogenic TrpRS sequences are useful as wound CC healing agents for re-vascularising damaged tissues. They are useful as wound CC treating full-thickness wounds (e.g. dermal ulcers, including pressure CC sequences can also be used in plastic surgery when reconstruction is CC required following a burn, other trauma, or even for cosmetic purposes. CC Angiogenic TrpRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft CC surgery and for repairing the damage of myocardial infarction and in CC conjunction with coronary bypass surgery by simulating the growth of CC transplanted tissue. TrpRS is also used in conjunction with angiography. CC promoting endothelialisation with angiography. CC promoting endothelialisation with angiography. CC myst shape antibodies may also be used to treat inflammation CC conjunction with coronary bypass surgery by simulating the growth of CC myst shape antibodies may also be used to treat inflammation CC conjunction with endotes may also be used to treat inflammation CC solid tumours. These antibodies may also be used to treat inflammation CC solid tumours to the activity and retard the growth of CC promoting the activity and preventing further growth of CC promoting the activity and retard the growth of CC promoting the activity of the conjunction with angiogenesis. The presence of tumours the activity of conjunction with angiogenesis. The presence is human truncated by conjunction with angiogenesis. The presence is human truncated conjunction in pET20B. discloses human aminoacyl tRNA synthetases,

Sequence 415 Æ

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The sequences given in AAB47615-18 show full length and truncated versions of trytophanyl-tRNA synthetase (TryRS). The truncated TryRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TryRS with polymorphonuclear leucocyte elastase. Truncated TryRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization;
decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans. It is also useful to the particular humans are particular humans. It is also useful to the particular humans and the particular humans are particular humans. It is also useful to the particular humans are particular humans and the particular humans are particular humans and the particular humans are part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 123-24; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schimmel P, Wakasugi K;
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Pred. No. 1
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domain;

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Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in

Example 1; Page 123-124; 149pp; English

CC truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann CC fold nucleotide binding domain and polynucleotides encoding them. The CC invention also relates to tyrosyl t-RNA synthetases (TyrRS). TrpRS CC sequences are useful for regulating vascular endothelial cell function, CC preferably angiogenesis. Angiogenic TypRS sequences are useful as wound CC healing agent for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure CC sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS CC sequences can also be used in plastic surgery when reconstruction is CC required following a burn, other trauma, or even for cosmetic purposes. CA Angiogenic TypRS is also used in association with surgery and following the damage of myocardial infarction and in CC conjunction with coronary bypass surgery by stimulating the growth of CC transplanted tissue. TrpRS is also used in conjunction with angiography. TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in CC immunoassays to detect the presence of tumours. They are also useful for process by antisense technology is useful for preventing further growth of CC caused by increased vascular permeability. Inhibiting the activity of CC repRS by antisense technology is useful for preventing further growth CC psoriasis, diabetic retinopathy, all of which are characterised by cabnormal angiogenesis. The present sequence is human truncated CC tryptophanyl t-RNA synthetase (mini TrpRS; residues 48-471 of cull-length TrpRS protein) protein in pET20B. aminoacyl tRNA synthetases, particularly

Sequence 437 AA;

Length 437;

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                                                                                 KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
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KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
                                                                KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
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Pred. No. 1.8e-209;
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SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP

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FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP

SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH

Matches

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                                                                                                                                                                                                                 decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the block access.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAB47615-18 show full length and truncated versions of trytophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or approach described a produced in the solid tumor increased or the solid tumor, and a condition that would benefit from increased or the solid tumor, and a condition that would benefit from increased or the solid tumor approach the solid tumor and a condition that would benefit from increased or the solid tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenesis; graft; myocardial infarction; solid tumour; wound dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
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                                                                                                                       Sequence
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    100.0%;
Score 2116; DB 22;
Pred. No. 2.1e-209;
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                                                                                                                                                                                                                                                                                                                                                                                                  Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in
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CC Angiogenic TrpRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft cc surgery and for repairing the damage of myocardial infarction and in cc conjunction with coronary bypass surgery by stimulating the growth of cc transplanted tissue. TrpRS is also used in conjunction with angiography. CC TrpRS DNAs are useful in gene therapy. TrpRs antibodies are useful in cc immunoassays to detect the presence of tumours. They are also useful cc for blocking endogenous angiogenic activity and retard the growth of cc solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of cropRS by antisense technology is useful for preventing further growth cc or even regress solid tumours, and for treating rheumatoid arthritis, cg psoriasis, diabetic retinopathy, all of which are characterised by cabnormal angiogenesis. The present sequence is human tryptophanyl cc abnormal angiogenesis. The present sequence is human tryptophanyl
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reproductive;

The patent discloses human aminoacyl tRNA synthetases, particularly truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann fold nucleotide binding domain and polynucleotides encoding them. The invention also relates to tyrosyl t-RNA synthetases (TyrRS). TrpRS sequences are useful for regulating vascular endothelial cell function, preferably angiogenesis. Angiogenic TrpRS sequences are useful as wound healing agents for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS sequences can also be used in plastic surgery when reconstruction is

21-SEP-2000 WO200055180-A2 Page 117-119; 149pp; English.

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h as lung /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous othe disgnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB5849 are used in the course of the invention for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated proteins represented in Ambourty fractions and associated proteins and polynucleotide sequences, their agonists, and associated proteins and polynucleotide cytostatic; cardioactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1052-1053; 1425pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung cancer associated gene sequences, referred antigens, useful for treatment, prevention, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identification and
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DB; AAF18096.
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                     KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
                                                                                    KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
                                                                                                                                                                                                       VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                       VVKIQKHVTENQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIFCA
                                                                                                                                                                                                                                                                      LVIQMTDDEKYLWKDLTLDQAYSYAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                                                                                                                                                                                           LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
KKALIEVL@PLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
                                                                                                                                    IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                                                                                                                                                                                                                                                                                                         FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIFFIFTKWLQDVFNVP
                                                                   KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characterisation of the polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2101; DB 21;
Pred. No. 7.1e-208;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF18424 encode human lung cancer
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diagnosis of disorders
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Best Local
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                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes
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08-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCMV inducible gene; cig; human; human
anti-viral therapy; anti-HCMV therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human HCMV inducible gene protein,
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                                                                                                                                                                                                                                    1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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                                                                                                                                                                                                                                                                                       Similarity
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                                                                     VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                            LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                                                               FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIFFIFTKWLQDVFNVP
               IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                                                                                                                                                        FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                                                                                                    SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                    VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                         LVIQMTDDEKYLWKDLTLDQAYSYAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                                                                                                                                                                                                                              471 AA;
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97US-0058180.
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Pred. No. 2.3e-207;
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detection; diagnosis;
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                                                                                                                                                                    decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic trNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graff; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization;
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 135-36; 150pp; English.
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Best Local Similarity

Score 1988; DB 22; Pred. No. 2.5e-196;

Length 392;

patent discloses human aminoacyl tRNA synthetases,

particularly

Query Match

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                                                Disclosure; Page 135-136; 149pp; English
                                                                                                                                 Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in
                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-193471P
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Matches 378
  pharmaceutical.
                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                   Drosophila melanogaster polypeptide SEQ ID NO 20655.
                                                                                                                                                                                                         ABB64621 standard; Protein; 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                ATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
                            VLQPLIAEHQARRKEVTDEIVKEFMTPRKLSF 398
                                                                              FSGGRDTIBEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALIE
                                                                                                                                    FRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHA
                                                                                                                                                                                CVTFNQVKGIFGFGDSDIIGKIGFPAAQAAPAISSTFPFIFGNR-KVHCLIPCAIDQDPY
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TLTPIVEQHQAARKLITDEVLDKYFELRPLKF
                                                           FSGGRVSVEEHRKLGGVPEVDVSYQLLKFFLEDDAKLEEVRVAYSKGEMLTGEIKKLAVE
                                                                                                                     FRMTRDVAPRLGFPKCALIHSTFFPALQGAKTKMSASDQNSAVYLTDTPKQIKNKINKYA
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Pred. No. 1.7e-132;
Pred. No. 1.7e-132;
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N-PSDB; ABL11306.
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11-JUL-2000; 2000US-0614150.
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                                                                                                      CVTFNQVKGIFGFGDSDIIGKIGFPAAQAAPAISSTFPFIFGNR-KVHCLIPCAIDQDFY
                                                                    HVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPY
                                                                                                                                                          FFSHRDLHTILTLREQGKPFYLYTGRGPSSGSLHVGHLVPFIMTKWLQETFDVPLVIQLT
                                                                                                                                                                            FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMT 126
                                                                                                                                                                                                                                ATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
                                                                                                                                                                                                                ATAPTEDVVDPWNVASSNDAGVDYDKLIKRFGSSKIDEELIARFEKITGKPAHHFIRRGM
FRMTRDVAPRLGFPKCALIHSTFFPALQGAKTKMSASDQNSAVYLTDTPKQIKNKINKYA
               FRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHA
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; Pred. No. 1.7e-132;
62; Mismatches 76;
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RESULT 13
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      WPI; 2001-201806/20
N-PSDB; AAF55855.
                                                                                                                               Tryptophanyl-tRNA
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                                                                                                      Candida albicans
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Query Match 57.6%; Sc Best Local Similarity 57.1%; Pr Matches 226; Conservative 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is Candida albicans cytoplasmic tryptophanyl-tRNA (ctRNA) synthetase. ctRNA synthetase is useful for producing recombinant ctRNA synthetases and detecting inhibitors of ctRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding Candida cytoplasmic tryptophanyl-tRNA (CtRNA) synthetases, useful for producing recombinant ctRNA synthetases and detecting inhibitor of Candida ctRNA synthetase function
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                                     ALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSF 398
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ECITVLQEFVSAYQERRSKVDDQVVEKFMKPHKLVF 406
                                                                                                                                       NKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKK 362
                                                                                                                                                                                                                                                     QDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKV 302
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                                                                                                          NKYAFSGGRATAEEHRELGGNPEVDVAFQYLSFFSYDDEKLAQLEQGYRKGEILSGEMKK 370
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